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L10: Entry 2 of 11

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Jun 17, 2004.

DOCUMENT-IDENTIFIER: US 20040115767 A1

TITLE: Immunogenic cell surface proteins of helicobacter pylori

Detail Description Paragraph:

[0073] Cell binding factor 2 (HP0175) has a similarity to cell-binding factor 2 of C jejuni (antigen PEB4A) and is a homologue to Escherichia coli survival protein surA. Here two were identified, but a further two-three isoforms with lower pI's could be proposed with the same M.sub.rs. Cross reactivity with serum from a C. jejuni infected patient was not observed.

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-
- 1. 5874300. 13 Mar 95; 23 Feb 99. Campylobacter jejuni antigens and methods for their production and use. Blaser; Martin J., et al. 435/325; 435/252.3 435/252.31 435/252.33 435/254.2 435/254.21 435/320.1 435/348 435/362 435/365 435/367 435/69.3 536/23.7. C12N015/31 C12N015/63 C12N015/70 C12N015/79.

 - 2. 5470958. 16 Sep 94; 28 Nov 95. Antisera against a PEB1 antigen from Campylobacter jejuni. Blaser; Martin J., et al. 530/389.5; 424/164.1 435/252.1 435/7.32 435/822. A61K035/16 A61K039/106.

 - 3. 5200344. 13 Nov 90; 06 Apr 93. Diagnostic testing for Campylobacter jejuni or Campylobacter coli infections using novel antigens. Blaser; Martin J., et al. 435/7.32; 435/29 435/7.92 435/961 435/967 436/547 530/389.5. G01N033/569.

Genes Dev. 1996 Dec 15;10(24):3170-82.

[Related Articles](#), [Links](#)

SurA, a periplasmic protein with peptidyl-prolyl isomerase activity, participates in the assembly of outer membrane porins.

Rouviere PE, Gross CA.

Department of Stomatology, University of California, San Francisco 94143-0512, USA.

Little is known about either the process of periplasmic protein folding or how information concerning the folding state in this compartment is communicated. We present evidence that SurA, a periplasmic protein with peptidyl-prolyl isomerase activity, is involved in the maturation and assembly of LamB. LamB is a trimeric outer membrane porin for maltodextrins as well as the bacteriophage lambda receptor in *Escherichia coli*. We demonstrate that SurA is involved in the conversion of unfolded monomers into a newly identified intermediate in LamB assembly, which behaves as a folded monomer. The absence of SurA blocks the assembly pathway and leads to accumulation of species prior to the folded monomer. These species also accumulate when the stress sigma factor sigmaE is induced by LamB overexpression. We suggest that accumulation of species prior to the generation of folded monomer is a stress signal sensed by sigmaE.

PMID: 8985185 [PubMed - indexed for MEDLINE]

Mol Microbiol. 1996 Aug;21(4):871-84.

[Related Articles](#), [Links](#)

New components of protein folding in extracytoplasmic compartments of *Escherichia coli* SurA, FkpA and Skp/OmpH.

Missiakas D, Betton JM, Raina S.

Centre Medical Universitaire, Departement de Biochimie Medicale, Geneve, Switzerland.

A global search for extracytoplasmic folding catalysts in *Escherichia coli* was undertaken using different genetic systems that produce unstable or misfolded proteins in the periplasm. The extent of misfolding was monitored by the increased activity of the sigma E regulon that is specifically induced by misfolded proteins in the periplasm. Using multicopy libraries, we cloned two genes, *surA* and *fkpA*, that decreased the sigma E-dependent response constitutively induced by misfolded proteins. According to their sequences and their biochemical activities, SurA and FkpA belong to two different peptidyl prolyl isomerase (PPI) families. Interestingly, *surA* was also selected as a multicopy suppressor of a defined *htrM* (*rfaD*) null mutation. Such mutants produce a defective lipopolysaccharide that is unable to protect outer membrane proteins from degradation during folding. The SurA multicopy suppression effect in *htrM* (*rfaD*) mutant bacteria was directly associated with its ability to catalyse the folding of outer membrane proteins immediately after export. Finally, Tn10 insertions were isolated, which led to an increased activity of the sigma E regulon. Such insertions were mapped to the *dsb* genes encoding catalysts of the protein disulphide isomerase (PDI) family, as well as to the *surA*, *fkpA* and *ompH/skp* genes. We propose that these three proteins (SurA, FkpA and OmpH/Skp) play an active role either as folding catalysts or as chaperones in extracytoplasmic compartments.

PMID: 8878048 [PubMed - indexed for MEDLINE]

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UniProtKB/Swiss-Prot entry P56112

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Entry information

Entry name	Y175_HELPY
Primary accession number	P56112
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 47, May 2005

Name and origin of the protein

Protein name	Hypothetical protein HP0175 [Precursor]
Synonyms	None
Gene name	OrderedLocusNames: HP0175
From	Helicobacter pylori (Campylobacter pylori) [TaxID: 210]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=26695 / ATCC 700392;

DOI=10.1038/41483; PubMed=9252185 [NCBI, ExPASy, EBI, Israel, Japan]

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., , Venter J.C.; "The complete genome sequence of the gastric pathogen Helicobacter pylori."; Nature 388:539-547(1997).

Comments

- **SIMILARITY:** Belongs to the ppiC/parvulin rotamase family.

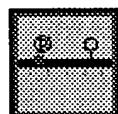
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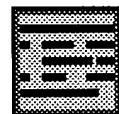
Cross-references

EMBL	AE000538; AAD07245.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	G64541; G64541.	
HSSP	P39159; 1JNS. [HSSP ENTRY / PDB]	
TIGR	HP0175; -. IPR000297; Rotamase.	

InterPro	Graphical view of domain structure.
Pfam	PF00639; Rotamase; 1. Pfam graphical view of domain structure.
PROSITE	PS01096; PPIC_PPIASE_1; 1. PS50198; PPIC_PPIASE_2; 1. PROSITE graphical view of domain structure (profiles).
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOGENOM	[Family / Alignment / Tree]
BLOCKS	P56112.
ProtoNet	P56112.
ProtoMap	P56112.
PRESAGE	P56112.
DIP	P56112.
ModBase	P56112.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords**Complete proteome; Hypothetical protein; Isomerase; Rotamase; Signal.****Features**

Feature table viewer



Feature aligner

Key	From	To	Length	Description
SIGNAL	1	21	21	Potential.
CHAIN	22	299	278	Hypothetical protein HP0175.
DOMAIN	154	253	100	PpiC.

Sequence information

Length: 299 AA [This is the length of the unprocessed precursor] Molecular weight: 34031 Da [This is the MW of the unprocessed precursor] CRC64: E65F3F2F94B11F5A [This is a checksum on the sequence]

10	20	30	40	50	60
MKKNILNLAL	VGALSTSFLM	AKPAHNANNA	THNTKTTDS	SAGVLATVDG	RPITKSDFDM
70	80	90	100	110	120
IKQRNPNFDF	DKLKEKEKEA	LIDQAIARTAL	VNEAKTEKL	DSTPEFKAMM	EAVKKQALVE
130	140	150	160	170	180
FWAKKQAEEV	KKVQIPEKEM	QDFYNANKDQ	LFVKQEAHAR	HILVKTEDEA	KRIISEIDKQ
190	200	210	220	230	240
PKAKKEAKFI	ELANRDTIDP	NSKNAQNGGD	LGKFQKNQMA	PDFSKAAFAL	TPGDYTKTPV
250	260	270	280	290	
KTEFGYHIIY	LISKDSPVTY	TYEQAKPTIK	GMLQEKLFOE	RMNQRIEELR	KHAKIVINK

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Dotlet (Java)



ScanProsite, MotifScan



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tools

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NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 299 AA (of which 8% low-complexity regions filtered out)

Date run: 2005-06-08 04:55:01 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,974,938 sequences; 640,866,274 total letters

UniProt Release 5.1 consists of: Swiss-Prot Release 47.1 of 24-May-2005: 181821 entries
TrEMBL Release 30.1 of 24-May-2005: 1748002 entries

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List of potentially matching sequences

Send selected sequences to

Include query sequence

Db	AC	Description	Score	E-value
<input checked="" type="checkbox"/>	sp_P56112	Y175_HELPY Hypothetical protein HP0175 precursor [HP01...	534	e-150
<input type="checkbox"/>	sp_Q9ZMQ7	Y175_HELPJ Hypothetical protein JHP0161 precursor [JHP...	523	e-147
<input type="checkbox"/>	tr_Q7VJY7	_HELHP Hypothetical protein [HH0105] [Helicobacter hepa...	225	1e-57
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<input checked="" type="checkbox"/>	sp_Q46105	CBF2_CAMJE Cell binding factor 2 precursor (Major anti...	138	1e-31
<input type="checkbox"/>	tr_Q5EVH4	_CAMJR Major antigenic peptide PEB4 [CJE0699] [Campylob...	138	1e-31
<input type="checkbox"/>	tr_Q8YJG0	_BRUME PEPTIDYL-PROLYL CIS-TRANS ISOMERASE [BMEI0123] [...	134	3e-30
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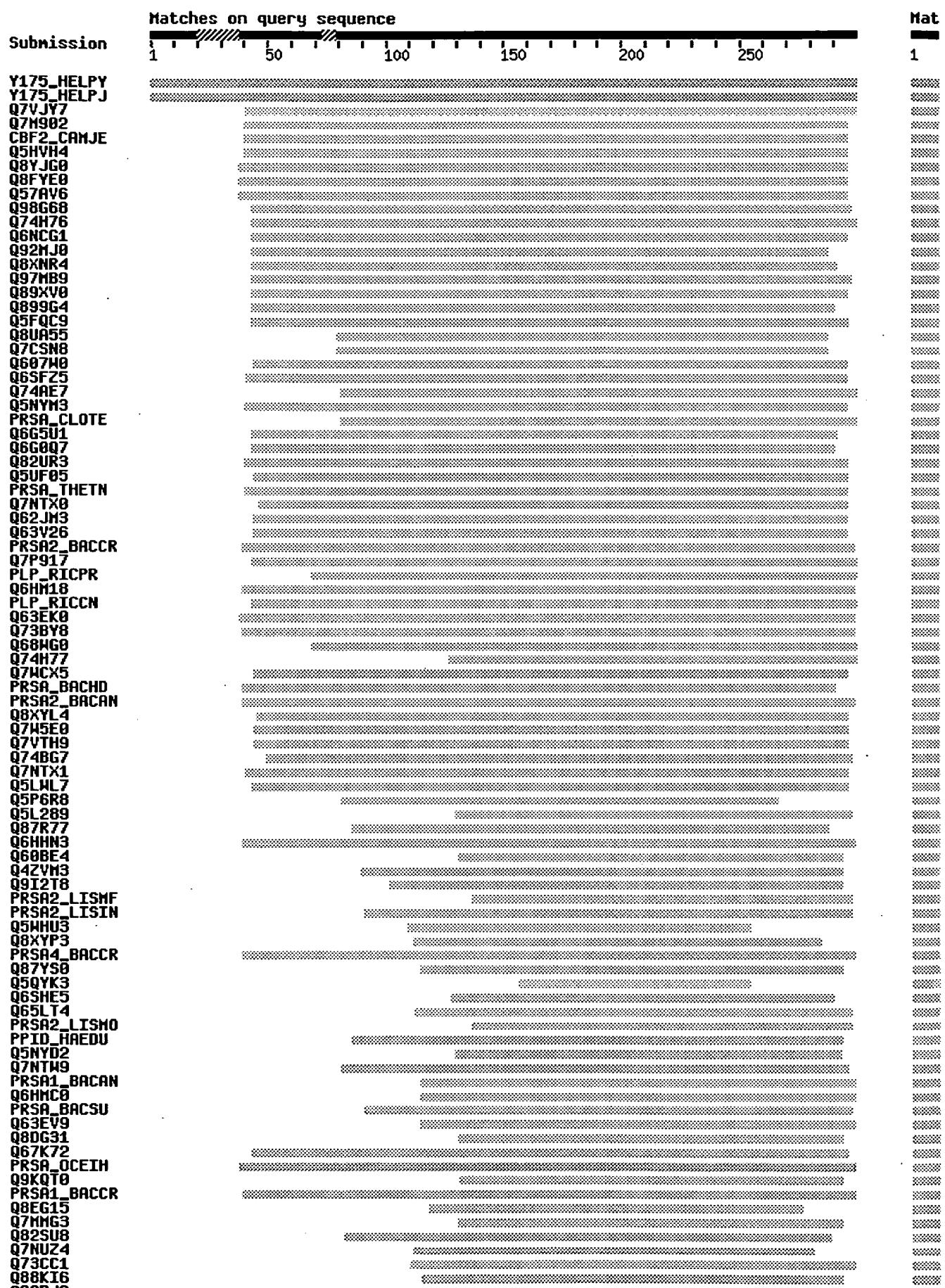
tr	<u>Q74H76</u>	GEOSL PPIC-type PPIASE domain protein [GSU0016] [Geobacillus...]	124	3e-27
tr	<u>Q6NCG1</u>	RHOPA PpiC-type peptidyl-prolyl cis-trans isomerase precursor [SPO0058] [Silicibacter sp. (strain Sili-1)]	123	4e-27
tr	<u>Q92MJ0</u>	RHIME PUTATIVE OUTER MEMBRANE PROTEIN [R02626] [Rhizobium...]	120	5e-26
tr	<u>Q8XNR4</u>	CLOPE Hypothetical protein CPE0268 [CPE0268] [Clostridium...]	117	4e-25
tr	<u>Q97MB9</u>	CLOAB Peptidyl-prolyl cis-trans isomerase [CAC0279] [Candida...]	116	5e-25
tr	<u>Q89XV0</u>	BRAJA Blr0205 protein [blr0205] [Bradyrhizobium japonicum...]	115	1e-24
tr	<u>Q899G4</u>	CLOTE Putative peptidyl-prolyl cis-trans isomerase [Candida...]	114	2e-24
tr	<u>Q5FQC9</u>	GLUOX Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)...	112	7e-24
tr	<u>Q8UA55</u>	AGR5 Peptidyl-prolyl cis-trans isomerase [ppiD] [Agrobacterium...]	111	2e-23
tr	<u>Q7CSN8</u>	AGR_L_2623p [AGR_L_2623] [Agrobacterium tumefaciens C58...]	111	2e-23
tr	<u>Q607W0</u>	METCA Peptidyl-prolyl cis-trans isomerase family protein [Bacillus...]	110	4e-23
tr	<u>Q6SFZ5</u>	9BACT PPIC-type PPIASE domain protein [EBAC080-L12H07]...	109	8e-23
tr	<u>Q74AE7</u>	GEOSL PPIC-type PPIASE domain protein [GSU2429] [Geobacillus...]	107	2e-22
tr	<u>Q5NYM3</u>	AZOSE PpiC-type peptidyl-prolyl cis-trans isomerase [Azotobacter...]	106	7e-22
sp	<u>Q899I2</u>	PRSA_CLOTE Foldase protein prsA precursor (EC 5.2.1.8)...	100	3e-20
tr	<u>Q6G5U1</u>	BARHE Peptidyl-prolyl cis-trans isomerase [BH02000] [Bacillus...]	100	4e-20
tr	<u>Q6G0Q7</u>	BARQU Peptidyl-prolyl cis-trans isomerase [BQ01880] [Bacillus...]	100	5e-20
tr	<u>Q82UR3</u>	NITEU PpiC-type peptidyl-prolyl cis-trans isomerase [Neisseria...]	99	1e-19
tr	<u>Q5UF05</u>	9PROT Predicted parvulin-like peptidyl-prolyl isomeras...	99	1e-19
sp	<u>Q8R760</u>	PRSA_THETN Foldase protein prsA precursor (EC 5.2.1.8)...	97	3e-19
tr	<u>Q7NTX0</u>	CHRVO Probable signal peptide protein (EC 5.2.1.8) [Candida...]	97	5e-19
tr	<u>Q62JM3</u>	BURMA Peptidyl-prolyl cis-trans isomerase domain protein [Burkholderia...]	94	4e-18
tr	<u>Q63V26</u>	BURPS Putative exported isomerase [BPSL1418] [Burkholderia...]	92	1e-17
sp	<u>Q81GN0</u>	PRSA2_BACCR Foldase protein prsA 2 precursor (EC 5.2.1.8)...	91	4e-17
tr	<u>Q7P917</u>	RICSI Protein export protein prsA precursor [rsib_orf00001]...	90	7e-17
sp	<u>Q9ZCX6</u>	PLP_RICPR Parvulin-like PPIase precursor (EC 5.2.1.8) ...	89	9e-17
tr	<u>Q6HM18</u>	BACHK Peptidyl-prolyl cis-trans isomerase (Protein export protein)...	89	9e-17
sp	<u>Q92H91</u>	PLP_RICCN Parvulin-like PPIase precursor (EC 5.2.1.8) ...	89	1e-16
tr	<u>Q63EK0</u>	BACZZ Peptidyl-prolyl cis-trans isomerase (Protein export protein)...	89	1e-16
tr	<u>Q73BY8</u>	BACCI Protein export protein prsA (EC 5.2.1.8) [prsA] ...	88	2e-16
tr	<u>Q68WG0</u>	RICTY Protein export protein PrsA [prsA] [Rickettsia typhi...]	87	3e-16
tr	<u>Q74H77</u>	GEOSL PPIC-type PPIASE domain protein [GSU0015] [Geobacillus...]	87	6e-16
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sp	<u>Q9KDN4</u>	PRSA_BACHD Foldase protein prsA precursor (EC 5.2.1.8)...	86	1e-15
sp	<u>Q81TU1</u>	PRSA2_BACAN Foldase protein prsA 2 precursor (EC 5.2.1.8)...	86	1e-15
tr	<u>Q8XYL4</u>	RALSO PUTATIVE ISOMERASE ROTAMASE SIGNAL PEPTIDE PROTEIN [Sphaerotilus...]	86	1e-15
tr	<u>Q7W5E0</u>	BORPA Putative peptidyl-prolyl cis-trans isomerase [Bacillus...]	86	1e-15
tr	<u>Q7VTH9</u>	BORPE Putative peptidyl-prolyl cis-trans isomerase [Bacillus...]	86	1e-15
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tr	<u>Q5L289</u>	GEOKA Post-translocation molecular chaperone [GK0656] ...	82	1e-14
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<input type="checkbox"/>	tr	Q5WHU3	BACSK	Protein export protein PrsA [prsA] [Bacillus cla...]	75	1e-12
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<input type="checkbox"/>	sp	Q81U45	PRSA1_BACAN	Foldase protein prsA 1 precursor (EC 5.2.1...)	73	8e-12
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<input type="checkbox"/>	tr	Q8EG15	SHEON	Peptidyl-prolyl cis-trans isomerase D [ppiD] [Sh...]	71	3e-11
<input type="checkbox"/>	tr	Q7MMG3	VIBVY	Parvulin-like peptidyl-prolyl isomerase [VV1108]...	71	3e-11
<input type="checkbox"/>	tr	Q82SU8	NITEU	PpiC-type peptidyl-prolyl cis-trans isomerase (E...)	70	4e-11
<input type="checkbox"/>	tr	Q7NUZ4	CHRVO	Probable peptidyl-prolyl cis-trans isomerase (EC...)	70	5e-11
<input type="checkbox"/>	tr	Q73CC1	BACC1	Protein export protein prsA (EC 5.2.1.8) [prsA] ...	70	5e-11
<input type="checkbox"/>	tr	Q88KI6	PSEPK	Peptidyl-prolyl cis-trans isomerase D, putative ...	70	7e-11
<input type="checkbox"/>	tr	Q6APJ9	DESPS	Related to peptidyl-prolyl cis-trans isomerase D....	69	9e-11
<input type="checkbox"/>	tr	Q72L30	THET2	Probable peptidyl-prolyl cis-trans isomerase (EC...)	69	9e-11
<input type="checkbox"/>	tr	Q65RG0	MANSM	SurA protein [surA] [Mannheimia succiniciproduc...]	69	1e-10
<input type="checkbox"/>	sp	Q81QT1	PRSA3_BACAN	Foldase protein prsA 3 precursor (EC 5.2.1...)	68	2e-10
<input type="checkbox"/>	tr	Q9CJM0	PASMU	Hypothetical protein PM1979 [PM1979] [Pasteurell...]	68	2e-10
<input type="checkbox"/>	tr	Q6HJ34	BACHK	Protein export protein prsA (EC 5.2.1.8) [prsA] ...	68	2e-10
<input type="checkbox"/>	tr	Q65PE9	BACLD	YacD [yacD] [Bacillus licheniformis (strain DSM ...)	68	2e-10
<input type="checkbox"/>	tr	Q63BM5	BACCZ	Protein export protein (EC 5.2.1.8) [prsA] [Baci...]	68	2e-10
<input type="checkbox"/>	tr	Q8H704	PHYIN	Peptidylprolyl isomerase [Phytophthora infestans...]	68	2e-10
<input type="checkbox"/>	tr	Q72D64	DESVH	Peptidyl-prolyl cis-trans isomerase domain protei...	68	3e-10
<input type="checkbox"/>	tr	Q62ZT8	BACLD	Putative PpiC-type peptidyl-prolyl cis-trans iso...	68	3e-10
<input type="checkbox"/>	sp	Q71ZM6	PRSA1_LISMF	Foldase protein prsA 1 precursor (EC 5.2.1...)	67	4e-10
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<input type="checkbox"/>	sp	Q02473	PRSA_LACPA	Foldase protein prsA precursor (EC 5.2.1.8)...	67	5e-10

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
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Profile hits  **PPIC_PPIASE_2**
Pfam hits  **Rotamase**



Alignments

sp P56112 Hypothetical protein HP0175 precursor [HP0175] 299
 Y175_HELPY [Helicobacter pylori
 (Campylobacter pylori)] AA align

Score = 534 bits (1375), Expect = e-150
 Identities = 275/299 (91%), Positives = 275/299 (91%)

Query: 1 MKKNILNLALVGALSTSFLMXXXXXXXXXXXXXXDSSAGVLATVDGRPITKSDFDM 60
 MKKNILNLALVGALSTSFLM DSSAGVLATVDGRPITKSDFDM

Sbjct: 1 MKKNILNLALVGALSTSFLMAKPAAHNANNATHNTKTTDSSAGVLATVDGRPITKSDFDM 60

Query: 61 IKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120

IKQRNPNFDFDKL ALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE

Sbjct: 61 IKQRNPNFDFDKLKEKEKEALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120

Query: 121 FWAKKQAEEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

FWAKKQAEEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ

Sbjct: 121 FWAKKQAEEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

Query: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGDLGKFQKNQMAPPDFSKAAFALT PGDYTKTPV 240

PKAKKEAKFIELANRDTIDPNSKNAQNGDLGKFQKNQMAPPDFSKAAFALT PGDYTKTPV

Sbjct: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGDLGKFQKNQMAPPDFSKAAFALT PGDYTKTPV 240

Query: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOERMNQRIEELRKHAKIVINK 299

KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOERMNQRIEELRKHAKIVINK

Sbjct: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOERMNQRIEELRKHAKIVINK 299

sp Q9ZMQ7 Hypothetical protein JHP0161 precursor [JHP0161] 299
 Y175_HELPJ [Helicobacter
 pylori J99 (Campylobacter pylori J99)] AA align

Score = 523 bits (1348), Expect = e-147
 Identities = 268/299 (89%), Positives = 272/299 (90%)

Query: 1 MKKNILNLALVGALSTSFLMXXXXXXXXXXXXXXDSSAGVLATVDGRPITKSDFDM 60
 MKKNILNLALVGALS FLIM DSSAGVLATVDGRPITKSDFDM

Sbjct: 1 MKKNILNLALVGALSASFLMAKPAAHNANNSTHNTKETTDASAGVLATVDGRPITKSDFDM 60

Query: 61 IKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120

IKQRNPNFDFDKL ALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE

Sbjct: 61 IKQRNPNFDFDKLKEKEKEALIEQAIRTALVENEAKAEKLNQTPEFKAMMEAVKKQALVE 120

Query: 121 FWAKKQAEEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

FWAKKQAEEVKK+QIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ

Sbjct: 121 FWAKKQAEEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

Query: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGDLGKFQKNQMAPPDFSKAAFALT PGDYTKTPV 240

PKAKKEAKFIELANRDTIDPNSKNAQNGDLGKFQKNQMAPPDFSKAAFALT PGDYTKTPV

Sbjct: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGDLGKFQKNQMAPPDFSKAAFALT PGDYTKTPV 240

Query: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOERMNQRIEELRKHAKIVINK 299

KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOERMNQRIEELRKHAKIVINK

Sbjct: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLQERMNQRIEELRKHAKIVINK 299

tr Q7VJY7 Hypothetical protein [HH0105] [Helicobacter hepaticus] 276 AA
Q7VJY7_HELHP

align

Score = 225 bits (573), Expect = 1e-57

Identities = 121/258 (46%), Positives = 161/258 (61%), Gaps = 1/258 (0%)

Query: 42 AGVLATVDGRPITKSDFDMIKQRNPNFDFDKLXXXXXXALIDQAIRTALENEAKTEKLD 101
A ATVDG IT D +++KQ PNF+++KL L++ I L+ AK EALD

Sbjct: 20 AKTYATVDGVAITDKDMEILKQSIPNPNYNKLSEQEKEMLINELINRQLILKAAKQEKLD 79

Query: 102 STPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARH 161
++ E+ + ++K L++ W EKQA + + + + Y N+ + F+ QG ARH

Sbjct: 80 TSKEYTDTINSIKDNLLIDLWTKKQANSTQVPTMNDQLRKIYQENEGE-FIDQEGKARH 138

Query: 162 ILVKTEDEAKRIISEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAP 221
ILVK+E EAK IT E+DK KAK EAKTELAN +IDP SK +NGGDLG F++ M P

Sbjct: 139 ILVKSESEAKEIIKELDKVGKAKAEAKFIELANAKSIDPASKQQKNGGDLGVFKRAGMDP 198

Query: 222 DFSKAFAFLTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLQER 281
FSKAFAF L PG YTK PV T+FGYHIIYL K F Y+ AK I+ ++ + Q

Sbjct: 199 MFSKAFAFDLKPGTYTKEPVLTQFGYHIIYLERKSEPKVIPYKDAKKIIENSIMQSIQGG 258

Query: 282 MNQRRIEELRKHAKIVINK 299

M Q+I+ ER AKI I K

Sbjct: 259 MMQKIQALRAKAKIKITK 276

tr Q7M902 CELL BINDING FACTOR 2 MAJOR ANTIGEN PEB4A [WS1281] 271
Q7M902_WOLSU [Wolinella
succinogenes]

AA

align

Score = 184 bits (466), Expect = 3e-45

Identities = 100/255 (39%), Positives = 152/255 (59%), Gaps = 7/255 (2%)

Query: 41 SAGVLATVDGRPITKSDFDMIKQRNPNFDFDKLXXXXXXALIDQAIRTALENEAKTEKL 100

SA IA+VDG IT D + + + P +D+L + + +QAI L+ +AK+E +

Sbjct: 21 SAKTLASVDGDEITDKDISVMLRAMPGVSYDQLPEDMQKKVLEQAIERKLLAKQAKSEGI 80

Query: 101 DSTPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHAR 160
++ EFK +E K+ +E W ++Q K + E +M+ FY+ NK++ + A+

Sbjct: 81 QNSKEFKDALEDAKEDELTVWVWRQQMNNAK--VSEGDMRKFYDENKEKFVQPELVKAK 137

Query: 161 HILVKTEDEAKRIISEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMA 220
HILV+E EAK +I+EI K AK KF EIA +IDP QNGG+LG F K+QM

Sbjct: 138 HILVQNEKEAKEVIAEIGKAG-AKASEKFSELAKSKSIDPAG--QNGGELGWFSKDQMV 193

Query: 221 PDFSKAFAFLTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLQFQE 280
P+F+ AAFAF G Y+KTYVKT+FGYH+TY K + YG KF I+ L+ + F++

Sbjct: 194 PEFANAAFAFLQKGSYSKTPVKTQFGYHVIYAEDKKAQAVLPYEDVKPQIEQNLKIQKFRD 253

Query: 281 RMNQRRIEELRKHAKI 295

++ ++IR+ A++

Sbjct: 254 SVSSTAKKLREKAQV 268

sp Q46105 Cell binding factor 2 precursor (Major antigen peb4A) 273
CBF2_CAMJE [cbf2] AA
[Campylobacter jejuni] align

Score = 138 bits (348), Expect = 1e-31
Identities = 88/256 (34%), Positives = 137/256 (53%), Gaps = 6/256 (2%)

Query: 41 SAGVLATVDGRPITKSDF-DMIKQRNPNFDFDKLXXXXXXALIDQAIRTA
LVEAKTEK 99
+A +ATV+G+ I+ ++ + DF L ALT Q I L+ +AK +
Sbjct: 20 NAATVATVNGKSISDTEVSEFFAPMLRGQDFKTLPDNQKKALIQQYIMQDLI
LQDAKKQN 79

Query: 100 LDSTPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQL
FVKQEAHA 159
L+ P + ++ K LV + +K +K I +++ FV+ NKD+ A
Sbjct: 80 LEKDPLYTKELDRAKDAILVN
VYQEKLNTIK---IDA
AKVAFYDQN
KDVKYVKPARVQA 136

Query: 160 RHILVKTEDEAKRIISEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNG
GDLGKFQKNQM 219
+HILV TE EAK II+E+ + +AKF EIA +IDP SKN GG+LG F ++ M
Sbjct: 137 KHILVATEKEAKDIIN
ELKGLKGKELDAKFS
ELAKEKSIDPGSKN--QGGELGWFDQSTM 194

Query: 220 APDFS KAAFALT
PGDYTKTPVKTEFGYHIIYLISKDS
PVTYTYEQA
KPTIKGMLQEKL
FQ 279
F+ AAFAL G T TFVET FGYR+I + + +++ K I+ L+ + F+
Sbjct: 195 VKPFT DAAFALKNGT
ITTPVKT
NFGYHVILKENS
QAKGQIKFDEV
KQGIENGLK
FEEFK 254

Query: 280 ERMNQRIEELRKHAKI 295
+ +NQ+ ++L AX+
Sbjct: 255 KVINQKGQDLLNSAKV 270

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UniProtKB/Swiss-Prot entry Q9ZK19

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Entry information

Entry name	EFTU_HELPJ
Primary accession number	Q9ZK19
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 39, May 2000
Sequence was last modified in	Release 39, May 2000
Annotations were last modified in	Release 47, May 2005

Name and origin of the protein

Protein name **Elongation factor Tu**

Synonym **EF-Tu**

Gene name

Name: tuf

Synonyms: tufA

OrderedLocusNames: JHP1128

From Helicobacter pylori J99 (Campylobacter pylori [TaxID: J99]) 85963]

Taxonomy Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

DOI=10.1038/16495; PubMed=9923682 [NCBI, ExPASy, EBI, Israel, Japan]

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Trust T.J.;

"Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";

Nature 397:176-180(1999).

Comments

- **FUNCTION:** This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis.
- **SUBUNIT:** Monomer (*By similarity*).
- **SUBCELLULAR LOCATION:** Cytoplasmic.
- **SIMILARITY:** Belongs to the GTP-binding elongation factor family. EF-Tu/EF-1A subfamily.

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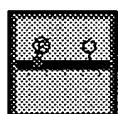
Cross-references

EMBL	AE001541; AAD06711.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	E71844; E71844.	
HSSP	P02990; 1ETU. [HSSP ENTRY / PDB]	
SMR	Q9ZK19; 5-399.	
CMR	Q9ZK19; JHP1128.	
HAMAP	MF_00118; -; 1. PBIL [Family / Alignment / Tree] IPR004541; EF-Tu. IPR004160; EFTU_Cterm. IPR004161; EFTU_D2. IPR000795; ProtSyn_GTPbind. IPR005225; Small_GTP. Graphical view of domain structure. PF00009; GTP_EFTU; 1.	
Pfam	PF03144; GTP_EFTU_D2; 1. PF03143; GTP_EFTU_D3; 1. Pfam graphical view of domain structure.	
PRINTS	PR00315; ELONGATNFCT.	
TIGRFAMs	TIGR00485; EF-Tu; 1. TIGR00231; small_GTP; 1.	
PROSITE	PS00301; EFACTOR_GTP; 1.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
BLOCKS	Q9ZK19.	
ProtoNet	Q9ZK19.	
ProtoMap	Q9ZK19.	
PRESAGE	Q9ZK19.	
DIP	Q9ZK19.	
ModBase	Q9ZK19.	
SWISS-2DPAGE	Get region on 2D PAGE.	
UniRef	View cluster of proteins with at least 50% / 90% identity.	

Keywords

Complete proteome; Elongation factor; GTP-binding; Protein biosynthesis.

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	19	26	8	GTP (By similarity).
NP_BIND	81	85	5	GTP (By similarity).
NP_BIND	136	139	4	GTP (By similarity).

Sequence information

Length: 399 Molecular weight: 43730 CRC64: 4E72A877BFCD104B [This is a checksum on the AA sequence]

10	20	30	40	50	60
MAKEKFNRTN	PHVNIGTIGH	VYHGKTTL	AISAVLSLKG	LAEMKDYDNI	DNAPQEKERG
70	80	90	100	110	120
ITIATSHIEY	ETETRHYAHV	DCPGHADYVK	NMITGAAQMD	GAILVVSAAD	GPMPQTREHI
130	140	150	160	170	180
LLSRQVGVP	HIVFLNKQDM	VDDQELLELV	EMEVRELLSA	YEFPGDDTP	VAGSALRALE
190	200	210	220	230	240
EAKAGNVGEW	GEKVLKLMAE	VDSYIPTPER	DTEKTFMLPV	EDVFSIAGR	TVVTGRIERG
250	260	270	280	290	300
VVKVGDEVEI	VGIRATQKTT	VTGVEMFRKE	LEKGEAGDNV	GVLLRGTKKE	EVERGMVLCK
310	320	330	340	350	360
PGSITPHKKF	EEEIYVLSKE	EGGRHTPFFT	NYRPQFYVRT	TDVTGSITLP	EGVEMVMPGD
370	380	390			
NVKITVELIS	PVALEGTKF	AIREGGRTVG	AGVVSNIIE		

Q9ZK19 in FASTA format

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ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-MODEL



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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 399 AA (of which 5% low-complexity regions filtered out)

Date run: 2005-06-08 05:58:30 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,974,938 sequences; 640,866,274 total letters

UniProt Release 5.1 consists of: Swiss-Prot Release 47.1 of 24-May-2005: 181821 entries
TrEMBL Release 30.1 of 24-May-2005: 1748002 entries

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List of potentially matching sequences

Send selected sequences to [Clustal W \(multiple alignment\)](#)

Include query sequence

Db	AC	Description	Score	E-value
----	----	-------------	-------	---------

<input checked="" type="checkbox"/>	sp Q9ZK19	EFTU_HELPJ Elongation factor Tu (EF-Tu) [tuf] [Helicob...	<u>743</u>	0.0
<input checked="" type="checkbox"/>	sp P56003	EFTU_HELPY Elongation factor Tu (EF-Tu) [tuf] [Helicob...	<u>728</u>	0.0
<input type="checkbox"/>	tr Q7VJ74	_HELHP Translation elongation factor EF-Tu (EC 3.6.1.48...)	<u>680</u>	0.0
<input checked="" type="checkbox"/>	sp P42482	EFTU_WOLSU Elongation factor Tu (EF-Tu) [tuf] [Wolinel...	<u>667</u>	0.0
<input checked="" type="checkbox"/>	sp O69303	EFTU_CAMJE Elongation factor Tu (EF-Tu) [tuf] [Campylo...	<u>637</u>	0.0
<input checked="" type="checkbox"/>	tr Q5HVZ7	_CAMJR Translation elongation factor Tu [tuf] [Campylob...	<u>637</u>	0.0
<input checked="" type="checkbox"/>	sp P64027	EFTU_NEIMB Elongation factor Tu (EF-Tu) [tufA] [Neisse...	<u>578</u>	e-164
<input checked="" type="checkbox"/>	sp P64026	EFTU_NEIMA Elongation factor Tu (EF-Tu) [tufA] [Neisse...	<u>578</u>	e-164
<input type="checkbox"/>	tr Q748X8	_GEOSL Translation elongation factor Tu [tuf-2] [Geobac...	<u>575</u>	e-163
<input type="checkbox"/>	tr Q5F5Q8	_NEIG1 Translation elongation factor TU [NGO1842] [Neis...	<u>575</u>	e-163

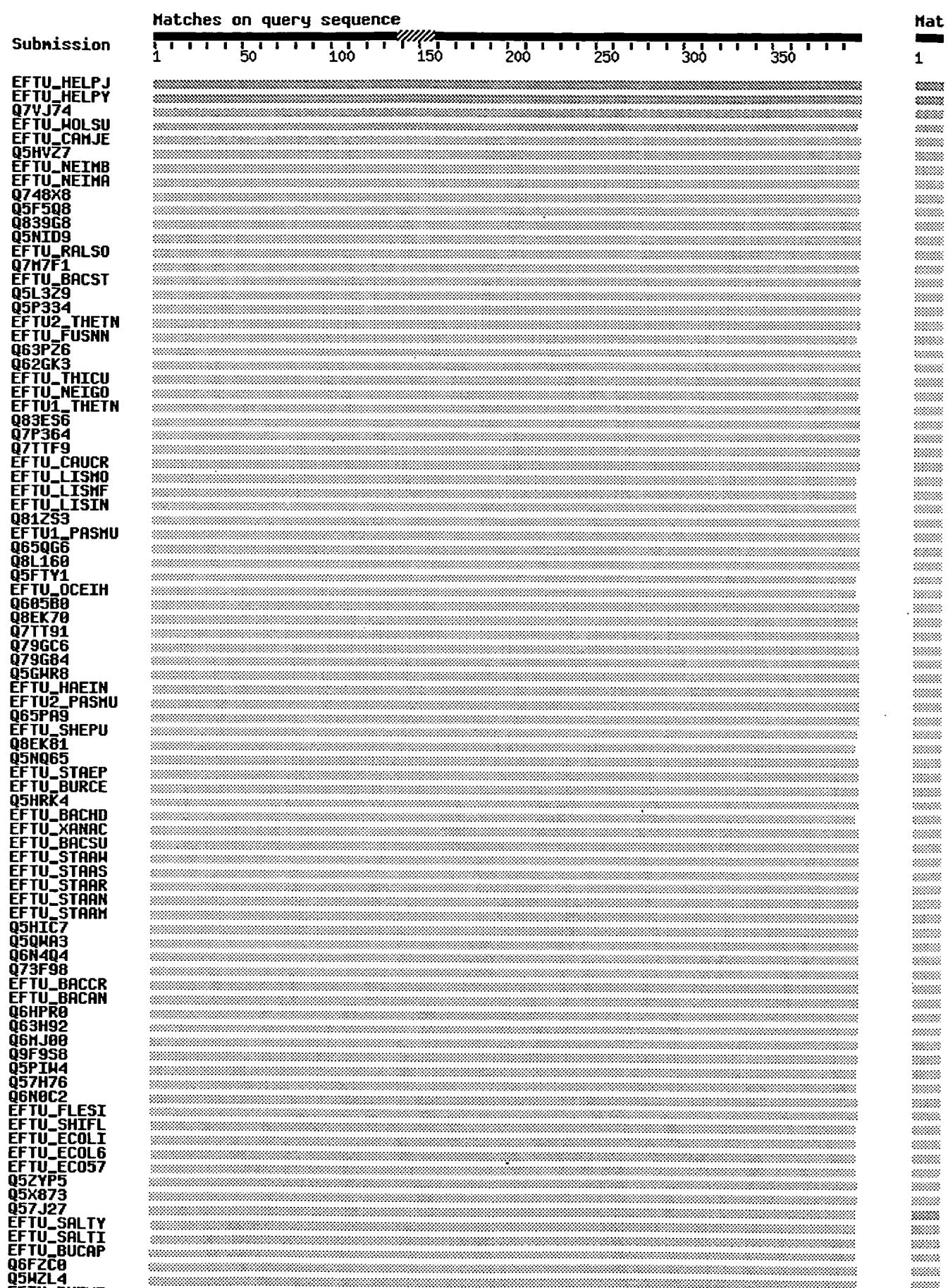
tr	<u>Q839G8</u>	_ENTFA	Translation elongation factor Tu [tuf]	[Enteroco...]	575	e-163	
tr	<u>Q5NID9</u>	_FRATT	Elongation factor Tu (EF-Tu)	[tufA]	[Francisella...]	574	e-162
sp	<u>Q8XGZ0</u>	EFTU_RALSO	Elongation factor Tu (EF-Tu)	[tufA]	[Ralsto...]	573	e-162
tr	<u>Q7M7F1</u>	_CHRVO	Translation elongation factor Tu (EC 3.6.1.48)	[...]	573	e-162	
sp	<u>Q50306</u>	EFTU_BACST	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...]	571	e-162
tr	<u>Q5L3Z9</u>	_GEOKA	Translation elongation factor Tu (EF-Tu)	[tufA]	[...]	570	e-161
tr	<u>Q5P334</u>	_AZOSE	Elongation factor Tu [tufB]	[Azoarcus sp. (strai...]	569	e-161	
sp	<u>Q8R7T8</u>	EFTU2_THETN	Elongation factor Tu-B (EF-Tu-B)	[tufB]	[T...]	568	e-161
sp	<u>Q8R603</u>	EFTU_FUSNN	Elongation factor Tu (EF-Tu)	[tuf]	[Fusobac...]	568	e-160
tr	<u>Q63PZ6</u>	_BURPS	Elongation factor Tu [tufA1]	[Burkholderia pseud...]	568	e-160	
tr	<u>Q62GK3</u>	_BURMA	Translation elongation factor Tu [tuf-1]	[Burkho...]	568	e-160	
sp	<u>P42481</u>	EFTU_THICU	Elongation factor Tu (EF-Tu)	[tuf]	[Thiobac...]	567	e-160
sp	<u>P48864</u>	EFTU_NEIGO	Elongation factor Tu (EF-Tu)	[tuf]	[Neisser...]	567	e-160
sp	<u>Q8R7V2</u>	EFTU1_THETN	Elongation factor Tu-A (EF-Tu-A)	[tufA]	[T...]	567	e-160
tr	<u>Q83ES6</u>	_COXBU	Translation elongation factor Tu [tuf-2]	[Coxiel...]	567	e-160	
tr	<u>Q7P364</u>	_FUSNV	Protein translation elongation factor Tu (EF-TU)	[...]	567	e-160	
tr	<u>Q7TTF9</u>	_HAEDU	Elongation factor tu, EF-Tu	[tufA]	[Haemophilus ...]	567	e-160
sp	<u>Q99QMO</u>	EFTU_CAUCR	Elongation factor Tu (EF-Tu)	[tufA]	[Caulob...]	566	e-160
sp	<u>Q8Y422</u>	EFTU_LISMO	Elongation factor Tu (EF-Tu)	[tuf]	[Listeri...]	566	e-160
sp	<u>Q71WB9</u>	EFTU_LISMF	Elongation factor Tu (EF-Tu)	[tuf]	[Listeri...]	566	e-160
sp	<u>Q927I6</u>	EFTU_LISIN	Elongation factor Tu (EF-Tu)	[tuf]	[Listeri...]	566	e-160
tr	<u>Q81ZS3</u>	_NITEU	GTPases-translation elongation factors and sulfat...	[...]	565	e-160	
sp	<u>P57939</u>	EFTU1_PASMU	Elongation factor Tu-A (EF-Tu-A)	[tufA]	[P...]	565	e-160
tr	<u>Q65QG6</u>	_MANSM	TufB protein [tufB]	[Mannheimia succiniciproduce...]	565	e-160	
tr	<u>Q8L160</u>	_MYXXA	Elongation factor Tu [tufA]	[Myxococcus xanthus]	565	e-160	
tr	<u>Q5FTY1</u>	_GLUOX	Protein Translation Elongation Factor Tu (EF-TU)	[...]	564	e-159	
sp	<u>Q8ETY4</u>	EFTU_OCEIH	Elongation factor Tu (EF-Tu)	[tuf]	[Oceanob...]	564	e-159
tr	<u>Q605B0</u>	_METCA	Translation elongation factor Tu [tuf-2]	[Methyl...]	563	e-159	
tr	<u>Q8EK70</u>	_SHEON	Translation elongation factor Tu [tufA]	[Shewanell...]	563	e-159	
tr	<u>Q7TT91</u>	_BORPE	Elongation factor Tu [tufA]	[Bordetella pertussis]	563	e-159	
tr	<u>Q79GC6</u>	_BORPA	Elongation factor Tu [tuf]	[Bordetella parapertu...]	563	e-159	
tr	<u>Q79G84</u>	_BORBR	Elongation factor Tu [tuf]	[Bordetella bronchise...]	563	e-159	
tr	<u>Q5GWR8</u>	_XANOR	Elongation factor Tu [tufB]	[Xanthomonas oryzae ...]	563	e-159	
sp	<u>P43926</u>	EFTU_HAEIN	Elongation factor Tu (EF-Tu)	[tufA]	[Haemop...]	562	e-159
sp	<u>P57966</u>	EFTU2_PASMU	Elongation factor Tu-B (EF-Tu-B)	[tufB]	[P...]	561	e-159
tr	<u>Q65PA9</u>	_BACLD	TufA (Elongation factor Tu)	[tufA]	[Bacillus lic...]	561	e-159
sp	<u>P33169</u>	EFTU_SHEPU	Elongation factor Tu (EF-Tu)	[tuf]	[Shewanell...]	561	e-158
tr	<u>Q8EK81</u>	_SHEON	Translation elongation factor Tu [tufB]	[Shewanell...]	561	e-158	
tr	<u>Q5NQ65</u>	_ZYMMO	Translation elongation factor [ZMO0516]	[Zymomon...]	561	e-158	
sp	<u>Q8CQ81</u>	EFTU_STAEP	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...]	560	e-158
sp	<u>P33167</u>	EFTU_BURCE	Elongation factor Tu (EF-Tu)	[tuf]	[Burkhol...]	560	e-158
tr	<u>Q5HRK4</u>	_STAEQ	Translation elongation factor Tu [tuf]	[Staphylo...]	560	e-158	
sp	<u>Q9Z9L6</u>	EFTU_BACHD	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...]	560	e-158
sp	<u>Q8NL22</u>	EFTU_XANAC	Elongation factor Tu (EF-Tu)	[tufA]	[Xantho...]	560	e-158
sp	<u>P33166</u>	EFTU_BACSU	Elongation factor Tu (EF-Tu) (P-40)	[tuf]	[...]	560	e-158

sp	P64029	EFTU_STAAW	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...]	559	e-158
sp	Q6GBT9	EFTU_STAAS	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...]	559	e-158
sp	Q6GJC0	EFTU_STAAR	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...]	559	e-158
sp	P99152	EFTU_STAAN	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...]	559	e-158
sp	P64028	EFTU_STAAM	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...]	559	e-158
tr	Q5HIC7	_STAAC	Translation elongation factor Tu	[tuf]	[Staphylo...]	559	e-158
tr	Q5QWA3	_IDILO	Translation elongation factor EF-Tu	[tufB_1]	[Id...]	559	e-158
tr	Q6N4Q4	_RHOPA	Elongation factor Tu (EC 3.6.1.48)	[tuf/ EF-Tu]	...	558	e-158
tr	Q73F98	_BACC1	Translation elongation factor Tu	[tuf]	[Bacillus...]	558	e-158
sp	Q814C4	EFTU_BACCR	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...]	558	e-158
sp	Q81VT2	EFTU_BACAN	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...]	558	e-158
tr	Q6HPRO	_BACHK	Protein-synthesizing GTPase (Translation elongat...			558	e-158
tr	Q63H92	_BACCZ	Protein-synthesizing GTPase (Translation elongat...			558	e-158
tr	Q6MJ00	_BDEBA	Translation elongation factor Tu (EC 3.6.1.48)	[...]		557	e-157
tr	Q9F9S8	_9PROT	Eftu [eftu]	[EDTA-degrading bacterium BN1]		557	e-157
tr	Q5PIW4	_SALPA	Elongation factor Tu [tufA]	[Salmonella paratyph...		556	e-157
tr	Q57H76	_SALCH	Protein chain elongation factor EF-Tu (Duplicate...			556	e-157
tr	Q6N0C2	_9PROT	EF-Tu [orf3309]	[Magnetospirillum gryphiswaldense]		556	e-157
sp	P26184	EFTU_FLESI	Elongation factor Tu (EF-Tu)	[tuf]	[Flexist...]	556	e-157
sp	Q83JC4	EFTU_SHIFL	Elongation factor Tu (EF-Tu)	[tufA]	[Shigel...]	555	e-157
sp	P0A6N1	EFTU_ECOLI	Elongation factor Tu (EF-Tu)	(P-43)	[tufA] ...	555	e-157
sp	P0A6N2	EFTU_ECOL6	Elongation factor Tu (EF-Tu)	(P-43)	[tufA] ...	555	e-157
sp	P0A6N3	EFTU_ECO57	Elongation factor Tu (EF-Tu)	(P-43)	[tufA] ...	555	e-157
tr	Q5ZYP5	_LEGPH	Translation elongation factor Tu (EF-Tu)	(EC 3.6...		555	e-157
tr	Q5X873	_LEGPA	Translation elongation factor Tu [tufA]	[Legione...]		555	e-157
tr	Q57J27	_SALCH	Protein chain elongation factor EF-Tu (Duplicate...			555	e-157
sp	P0A1H5	EFTU_SALTY	Elongation factor Tu (EF-Tu)	[tufA]	[Salmon...]	555	e-157
sp	P0A1H6	EFTU_SALTI	Elongation factor Tu (EF-Tu)	[tufA]	[Salmon...]	555	e-157
sp	O31298	EFTU_BUCAP	Elongation factor Tu (EF-Tu)	[tuf]	[Buchner...]	555	e-157
tr	Q6FZC0	_BARQU	Elongation factor tu (EF-tu)	[tuf1]	[Bartonella ...]	555	e-157
tr	Q5WZL4	_LEGPL	Elongation factor Tu [tufA]	[Legionella pneumoph...]		555	e-157
sp	Q925Y6	EFTU_RHIME	Elongation factor Tu (EF-Tu)	[tufA]	[Rhizob...]	554	e-156
tr	Q6FZL2	_BARQU	Elongation factor tu (EF-tu)	[tuf2]	[Bartonella ...]	554	e-156
tr	Q7MYE8	_PHOLL	Elongation factor Tu (EF-Tu)	[tufA]	[Photorhabdu...]	554	e-156
sp	P18668	EFTU_SYN6	Elongation factor Tu (EF-Tu)	[tuf]	[Synecho...]	554	e-156
sp	O31297	EFTU_BUCAI	Elongation factor Tu (EF-Tu)	[tuf]	[Buchner...]	554	e-156
sp	P33165	EFTU_BACFR	Elongation factor Tu (EF-Tu)	[tuf]	[Bactero...]	553	e-156
sp	P33171	EFTU_SYN7	Elongation factor Tu (EF-Tu)	[tuf]	[Synecho...]	553	e-156
sp	Q8ZAN8	EFTU2_YERPE	Elongation factor Tu-B (EF-Tu-B)	[tufB]	[Y...]	553	e-156
tr	Q66FQ9	_YERPS	Elongation factor Tu [tufA]	[Yersinia pseudotube...]		553	e-156
tr	Q8KHX9	_BARHE	Elongation factor TU (EF-Tu)	[tufB]	[Bartonella ...]	552	e-156
tr	Q89J82	_BRAJA	Elongation factor TU [tuf]	[Bradyrhizobium japon...]		552	e-156
tr	Q727D5	_DESVH	Translation elongation factor Tu [tuf]	[Desulfov...]		552	e-156
tr	Q7N9B1	_PHOLL	Translation elongation factor EF-Tu.B [tufB]	[Ph...]		552	e-156
sp	Q8UE16	EFTU_AGRT5	Elongation factor Tu (EF-Tu)	[tufA]	[Agroba...]	551	e-156

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits**Pfam hits**[GTP_EFTU](#)[GTP_EFTU_D2](#)[GTP_EFTU_D3](#)



Alignments

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sp Q9ZK19      Elongation factor Tu (EF-Tu) [tuf] [Helicobacter pylori] 399
EFTU_HELPJ J99
(Campylobacter pylori J99) ] AA align

Score = 743 bits (1919), Expect = 0.0
Identities = 378/399 (94%), Positives = 378/399 (94%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG
Sbjct: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60

Query: 61 ITIATSHIEYETETRHYAHDVCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
        ITIATSHIEYETETRHYAHDVCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
Sbjct: 61 ITIATSHIEYETETRHYAHDVCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LLSRQVGVPHVFLNK                               SAYEFPGDDTPIVAGSALRALE
Sbjct: 121 LLSRQVGVPHVFLNKQDMVDDQELLELVEMEVRELLSAYEFPGDDTPIVAGSALRALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
        EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG
Sbjct: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK
Sbjct: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
        PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD
Sbjct: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE
Sbjct: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

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sp P56003      Elongation factor Tu (EF-Tu) [tuf] [Helicobacter pylori] 399 AA
EFTU_HELPY (Campylobacter pylori) ] align

Score = 728 bits (1880), Expect = 0.0
Identities = 371/399 (92%), Positives = 373/399 (92%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG
Sbjct: 1 MAKEKFNRTKPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60

Query: 61 ITIATSHIEYETETRHYAHDVCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
        ITIATSHIEYETETRHYAHDVCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
Sbjct: 61 ITIATSHIEYETENRHYAHDVCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LLSRQVGVPHVFLNK                               SAYEFPGDDTPIVAGSALRALE

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Sbjct: 121 LLSRQVGPHIVVFLNKQDMVDDQELLELVELEMVERLLSAYEFPGDDTPIVAGSALRALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG

Sbjct: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK 300
VVKVGDEVEIVGIR TQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK

Sbjct: 241 VVKVGDEVEIVGIRPTQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD

Sbjct: 301 PGSITPHKKFEGEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE

Sbjct: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

tr Q7VJ74 Translation elongation factor EF-Tu (EC 3.6.1.48) [tufA] 399 AA
Q7VJ74_HELHP [Helicobacter hepaticus]

align

Score = 680 bits (1755), Expect = 0.0
Identities = 341/399 (85%), Positives = 360/399 (89%)

Query: 1 MAKEKFNRTPHNIGTIGHVYHGKTLSSAAISAVLSLKGLAEMKDYNIDNAPQEKEKRG 60
MAKEKF + PHVN+GTIGHV HGKTLSSAAISAVL+ KGLAE + KDYNIDNAP+EKEKRG

Sbjct: 1 MAKEKFVKNKPHNVNGTIGHVDHGKTLSSAAISAVLATKGLAELKDYNIDNAPEEKERG 60

Query: 61 ITIATSHIEYETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITIATSHIEYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITIATSHIEYETENRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LLSRQVGV +IVVFLNK S Y+FFGDDTP+AGSAL+ALE

Sbjct: 121 LLSRQVGVHYIVVFLNKQDMVDDAELLELVELEMVERLLSAYEFPGDDTPIIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG

Sbjct: 181 EAKAGNVGEWGEKVLKLMEVDKYIPTPQRDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK 300
VV+VGDEVEIVGIR TQKTTVTGVEMFRKELEKGEAGDNVG+LLRGTKKEEVERGMVLCK

Sbjct: 241 VVQVGDEVEIVGIRDQKTTVTGVEMFRKELEKGEAGDNVGILLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD

Sbjct: 301 PGSITPHKKFEGEIYVLSKDEGGRHTPFFNGYRPQFYVRTTDVTGSIELPSGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE

Sbjct: 361 NVKITVELIAPVALEDGTRFAIREGGRTVGSGVVTKIIE 399

sp P42482 Elongation factor Tu (EF-Tu) [tuf] [Wolinella EFTU_WOLSU succinogenes] 399 AA align

Score = 667 bits (1720), Expect = 0.0
 Identities = 337/397 (84%), Positives = 353/397 (88%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF + PHVNIGTIGHV HGKTTLSSAISAVL+ KGL S+KDYD IDNAP+E+ERG

Sbjct: 1 MAKEKFVKNKPHVNIGTIGHVDHGKTLSSAISAVLATKGLCELKYDAIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITIATSHIEYETE RHYAHDCPGHADYVRNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITIATSHIEYETENRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFLNK S Y+FFGDDTPIVAGSAL+ALE

Sbjct: 121 LLSRQVGVPYIVVFLNKEDMVDDAELLELVEMEVRELLSNYDFPGDDTPIVAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVTGRIERG 240
 EAK GNVGEWGEKVLKLMAEV D YIPTPERD +K FLMPVEDVFSIAGRGTVTGRIERG

Sbjct: 181 EAKTGNVGEWGEKVLKLMAEVDRYIPTPERDVDPFLMPVEDVFSIAGRGTVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VVKVGDEVEIVGIR TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKE+VERGMVLCK

Sbjct: 241 VVKVGDEVEIVGIRNTQKTTVTGVEMFRKELDKGEAGDNVGVLLRGTKKEDVERGMVLCK 300

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 GSITPH FE E+YVLSKEEGGRHTPFT YRPQFYVRTTDVTGSI+LPEGVEMVMPGD

Sbjct: 301 IGSITPHTNFEGEVYVLSKEEGGRHTPFNGYRPQFYVRTTDVTGSISLPEGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
 NVKI VELI+PVALE GT+FAIREGGRTVGAGVV+ I

Sbjct: 361 NVKINVELIAPVALEEGTRFAIREGGRTVGAGVVTKI 397

sp O69303 Elongation factor Tu (EF-Tu) [tuf] [Campylobacter jejuni] 399 AA
EFTU_CAMJE align

Score = 637 bits (1644), Expect = 0.0
 Identities = 315/399 (78%), Positives = 350/399 (86%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R PHVNIGTIGHV HGKTTLSSAISAVL+ KGL S+KDYD IDNAP+E+ERG

Sbjct: 1 MAKEKFSRNKPHVNIGTIGHVDHGKTLTAAISAVLSRRGLAELKDYNIDNAPPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITIATSHIEYET+ RHYAHDCPGHADYVRNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITIATSHIEYETDNRHYAHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFP+NK S+Y+FFGDDTPI++GSAL+ALE

Sbjct: 121 LLSRQVGVPYIVVFMNKADMVDDAELLELVEMEIRELLSSYDFPGDDTPIIISGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVTGRIERG 240
 EAKAG GEW K++ LMA VDSYIPTP RDTEK FLMP+EDVFSI+GRGTVTGRIE+G

Sbjct: 181 EAKAGQDGEWSAKIMDLMAAVDSYIPTPTRDTEKDFLMPIEDVFSISGRGTVVTGRIEK 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
VVKGVD +EIVGI+ TQ TTVTGVEMFRKE+++GEAGDNVGVLLRGTKKEEV RGMVL K

Sbjct: 241 VVKVGDTIEIVGIKDTQTTVTGVEMFRKEMDQGEAGDNVGVLLRGTKKEEVIRGMVLAK 300

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFNTYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
P SITPH FE E+Y+L+K+EGGRHTPF NYRPQFYVRTTDVTGSI L +GVEMVMPG+

Sbjct: 301 PKSITPHTDFEAEVYILNKDEGGRHTPFNNYRPQFYVRTTDVTGSIKLADGVEMVMPGE 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
NV+ITV LI+PVALE GT+FAIREGG+TVG+GVVS II+

Sbjct: 361 NVRITVSLIAPVALEEGRTRFAIREGGKTVGSGVVSIIK 399

tr Q5HVZ7 Translation elongation factor Tu [tuf] [Campylobacter] 399
Q5HVZ7_CAMJR jejuni AA
(strain RM1221) align

Score = 637 bits (1644), Expect = 0.0

Identities = 315/399 (78%), Positives = 350/399 (86%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNIDNAPQEKEKRG 60
MAKEKF+R PHVNIGTIGHV HGKTTL+AAISAVLS +GLAE+KDYNIDNIDNAP+EKEKRG

Sbjct: 1 MAKEKFSRNKPVNIGTIGHVDHGKTTLAAISAVLSRRGLAELKDYNIDNIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHVDCTPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITIATSHIEYET+ RHYANVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITIATSHIEYETDNRHYAHVDCTPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVVFNLKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LLSPQVGVP+TVVF+WK S+Y+FPGDDTPI++GSAI+ALE

Sbjct: 121 LLSRQVGVPYIVVFMNKADMVDDAELLELVEIMEIRELLSSYDFPGDDTPIISGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIERG 240
EAKAG GEW K++ LMA VDSYIPTP RDTEK FLMP+EDVFSI+GRGTVVTGRIE+G

Sbjct: 181 EAKAGQDGEWSAKIMDLMAAVDSYIPTPTRDTEKDFLMPIEDVFSISGRGTVVTGRIEK 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
VVKGVD +EIVGI+ TQ TTVTGVEMFRKE+++GEAGDNVGVLLRGTKKEEV RGMVL K

Sbjct: 241 VVKVGDTIEIVGIKDTQTTVTGVEMFRKEMDQGEAGDNVGVLLRGTKKEEVIRGMVLAK 300

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFNTYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
P SITPH FE E+Y+L+K+EGGRHTPF NYRPQFYVRTTDVTGSI L +GVEMVMPG+

Sbjct: 301 PKSITPHTDFEAEVYILNKDEGGRHTPFNNYRPQFYVRTTDVTGSIKLADGVEMVMPGE 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
NV+ITV LI+PVALE GT+FAIREGG+TVG+GVVS II+

Sbjct: 361 NVRITVSLIAPVALEEGRTRFAIREGGKTVGSGVVSIIK 399

sp P64027 Elongation factor Tu (EF-Tu) [tufA] [Neisseria] 394
EFTU_NEIMB meningitidis AA
(serogroup B) align

Score = 578 bits (1490), Expect = e-164
 Identities = 284/398 (71%), Positives = 331/398 (82%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF R+ PAVN+GTIGHV HGKTTL+AA++ +L+ K K YD IDNAP+EK RG
 Sbjct: 1 MAKEKFERSKPHNVNGTIGHVDHGKTLTAALTTILAKKFGGAAKAYDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EYETETRHAYHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITINTSHVEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VF+NK S+Y+FPGDD PIV GSAL+ALE
 Sbjct: 121 LLARQVGVPYIIVFMNKCDMVDDAELLELVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 A + EK+ +L A +DSYIPTPER +K FL+F+EDVFSI+GRGTVTGCR+ERG
 Sbjct: 181 GDAA----YEEKIFELAAALDSYIPTPERAVDKPFLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++ VGDE+EIVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL K
 Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PG+ITPH KF+ E+YVLSKEEGGRHTPFFT NYRPQFY RTTDTG++TL EGVEMVMPG+
 Sbjct: 296 PGTITPHTKFKAEVYVLSKEEGGRHTPFANYRPQFYRTTDVTGAVTLEEGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++T
 Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSSVI 393

sp <u>P64026</u>	Elongation factor Tu (EF-Tu) [tufA] [Neisseria	394
EFTU_NEIMA	meningitidis	AA
	(serogroup A)]	<u>align</u>

Score = 578 bits (1490), Expect = e-164
 Identities = 284/398 (71%), Positives = 331/398 (82%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF R+ PAVN+GTIGHV HGKTTL+AA++ +L+ K K YD IDNAP+EK RG
 Sbjct: 1 MAKEKFERSKPHNVNGTIGHVDHGKTLTAALTTILAKKFGGAAKAYDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EYETETRHAYHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITINTSHVEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VF+NK S+Y+FPGDD PIV GSAL+ALE
 Sbjct: 121 LLARQVGVPYIIVFMNKCDMVDDAELLELVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 A + EK+ +L A +DSYIPTPER +K FL+F+EDVFSI+GRGTVTGCR+ERG
 Sbjct: 181 GDAA----YEEKIFELAAALDSYIPTPERAVDKPFLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

++ VGDE+ELVG++ TQKTT TGVEMFRK L++G+AGDNVGVLRLRGTK+E+VERG VL K
 Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEQAGDNVGVLRLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PG+ITPH KF+ E+YVLSKEEGGRHTPFFT NYRPQFY RTTDVTG++TL EGVE/MVMPG+
 Sbjct: 296 PGTITPHTKFKAEVYVLSKEEGGRHTPFFANYRPQFYFRTTDVTGAVTLEEGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGKFAIREGGRTVGAGVVSNII 398
 NV ITVELI+P+A+E G +FAIREGGRTVGAGVVSS++T
 Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSSVI 393

tr Q748X8 Translation elongation factor Tu [tuf-2] [Geobacter 396
Q748X8_GEOSL sulfurreducens] AA
align

Score = 575 bits (1482), Expect = e-163
 Identities = 285/400 (71%), Positives = 328/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEFNRTNPVNIGTIGHVYHGKTLAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAX KF RT PHVNIGTIGHV HGKTTL+AAI+ VL+ +G AE + +D IDNAP+E+ERG
 Sbjct: 1 MAKAKFERTKPHVNIGTIGHVDHGKTLAAITKVLAERGQAEFRGFDQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITIATSH+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITIATSHVEYETEKRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+IVVFLNK S+Y+FPGDD PI+ GSAL+ L
 Sbjct: 121 LLARQVGVPVYIVVFLNKADMVDEELLEIRELSSYDFPGDDIPIIKGSALKGLN 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ E GE+ +IKIM VD+YIP PER +K FLMPVEDVFSI+GRGTV TGR+EK
 Sbjct: 181 ----GDKDELGEEAILKLMEAVDNYIPEPERAVDKPFLMPVEDVFSISGRGTVATGRVER 236

Query: 240 GVVKGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLC 299
 G+VKVG+EVEIVGI+AT KTTVTGVEMFRK L++G AGDN+G LIIG K+E++ERG VL
 Sbjct: 237 GIVKGEEVEIVGIKATAKTTVTGVEMFRKLLDEGRAGDNIGALLRGVKREDIERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVPG 359
 KPGSITPH KF+ E Y+L+KEEGGRHTPFFT VRPQFY RTTDVTG + LP G EMVMPG
 Sbjct: 297 KPGSITPHTKFKAEEAYILTKEEGGRHTPFFNGYRPQFYFRTTDVTGVVDPAGTEMVMPG 356

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIIE 399
 DNV +T+ LI+P+A++ G +FAIREGGRTVGAGVVSS+IE
 Sbjct: 357 DNVAVTINLITPIAMDEGLRFAIREGGRTVGAGVVSSIIE 396

tr Q5F5Q8 Translation elongation factor TU [NGO1842] [Neisseria 394
Q5F5Q8_NEIG1 gonorrhoeae AA
(strain ATCC 700825 / FA 1090) align

Score = 575 bits (1482), Expect = e-163
 Identities = 282/398 (70%), Positives = 330/398 (82%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF R+ PHVN+GTLGHV HGKTTL+AAT++ VLS K K YD IDNAP+EK RG
 Sbjct: 1 MAKEKFERSKPHVNVTIGHVDHGKTTLAALTTI LAKKFGGAAKAYDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+YETETRHAYHDCPGHADYVKNMITGAAQMDGAILVV SAADGPMPQTREHI
 Sbjct: 61 ITINTSHVEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+PQVGVP+I+VF+NK S+Y+FPGDD PIV GSAL+ALE
 Sbjct: 121 LLARQVGVPYIIVFMNKCDMVDDAELLELVEMEIRDLSSYDFPGDDCPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 A + EK+ +L +DSYIPTPER +K FL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 GDAA----YEKIFELATALDSYIPTPERAVDKPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++ VGDE+EIVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL K
 Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PG+ITPH KF+ E+YVLSKEEGGRHTPFT NYRPQFY RTPDVTG++TL +GVEMVMPGD
 Sbjct: 296 PGTITPHTKFKAEVYVLSKEEGGRHTPFANYRPQFYRTTDVTGAVTLEKGVEMVMPGE 355

Query: 361 NVKITVELISPVALEGTKFAIREGGRTVGAGVVSNII 398
 NV ITVELI+F+A+E G +FAIREGGRTVGAGVVSS++I
 Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSSVI 393

tr Q839G8	Translation elongation factor Tu [tuf] [Enterococcus	395
Q839G8_ENTFA	faecalis	AA
	(Streptococcus faecalis)]	<u>align</u>

Score = 575 bits (1481), Expect = e-163
 Identities = 288/400 (72%), Positives = 328/400 (82%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF+R+ HVNIGTIGHV HGKTTL+AAT+ VLS G E + YD+IDNAP+EKRG
 Sbjct: 1 MAKEKFDRSKSHVNIGTIGHVDHGKTTAAIATVLSKHGGEAQSYDSIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVV SAADGPMPQTREHI
 Sbjct: 61 ITINTSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+PQVGVP+I+VF+LNK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPYIIVFLNKCDMVDDAELLELVEMEIRDLSSYDFPGDDCPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 + + EK+L+LMA VD YIPTPERDT+K F+MPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 GDES----YEKILELMAAVDEYIPTPERDTDKPMMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIR-ATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 299
 V+VGDEVEIVG+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E++ERG VL
 Sbjct: 236 EVRVGDEVEIVGIKDETSLKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIERGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KP +TPH KF+ E+YVLSKEEGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMPG
 Sbjct: 296 KPATITPHTKFKAEVYVLSKEEGGRHTPFFTNYRPQFYFRTTDVTGVVELPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIE 399
 DNV + VELI P+A+E GT+F+IREGGRTVG+GVV+ I++
 Sbjct: 356 DNVAMDVELIHPIAIEDGTRFSIREGGRTVGSGVVTEIVK 395

tr Q5NID9 Elongation factor Tu (EF-Tu) [tufA] [Francisella
Q5NID9_FRATT tularensis (subsp.
 tularensis)] 394
 AA
align

Score = 574 bits (1480), Expect = e-162
 Identities = 281/399 (70%), Positives = 328/399 (81%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF RT PHVN+GTIGHV HGKTL+AAI+ V++ K + ID AP+EK RG
 Sbjct: 1 MAKEKFERSKPHVNVTIGHVDHGKTTLAAITKVMMAEKNGGMARKFDEIDSAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGPMPQTREHI 120
 ITI TSH+EYB+ RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITINTSHVEYESPNRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP HVFLNK YEEFPGDDTP++ GSALRA+E
 Sbjct: 121 LLSRQVGVPKIVVFLNKCDMVDDDEELLELVEMEVRELLDQYEPFGDDTPVIMGSALRAIE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 +A + EK+++I+ +D YIP PERDTEK F++P+EDVFSI+GRGTVVTGRIERG
 Sbjct: 181 GDEA----YVEKIVELVQAMDDYIPAPERDTEKPFILPIEDVFSISGRGTVVTGRIERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VV +GDEVE+VGIR TQKTTVTGVEMFRK L++GEAGDNVG+L+RG K+++VERG VLCK
 Sbjct: 236 VVNIGDEVEVVGIRPTQKTTVTGVEMFRKLLDRGEAGDNVGILVRGLKRDDVERGQLCK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PH KF+ E+YVLSKEEGGRHTPFFT YRPQFY RTTD+TG++ LPEGVEMVMPGD
 Sbjct: 296 PGSIKPHTKFEAEVYVLSKEEGGRHTPKGYRPQFYFRTTDITGAVELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIE 399
 NVK+T+ LI+P+A++ G +FAIREGGRTVGAGVV+ ITE
 Sbjct: 356 NVKMTITLINPIAMDEGLRFAIREGGRTVGAGVVAKIIE 394

sp Q8XGZ0 Elongation factor Tu (EF-Tu) [tufA] [Ralstonia
EFTU_RALSO solanacearum
 (Pseudomonas solanacearum)] 396
 AA
align

Score = 573 bits (1477), Expect = e-162
 Identities = 289/400 (72%), Positives = 327/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF RT PHVN+GTIGHV HGKTL+AAI+ VLS K E K YD ID AP+EK RG
 Sbjct: 1 MAKEKFERTKPHVNVTIGHVDHGKTTLAAITVLSSKFGGEAKKYDEIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+NIEYET RHYAHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITINTAHIEYETANRHAYHDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTP+ GSA ALE
 Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDAELLELVELEMVERLLSKYDFPGDDTPIIKGSAKLALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTLMPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE + +A+ +DSYIPTPER + TFLMPVEDVFSI+GRGTVVTGRIER
 Sbjct: 181 ----GDKGELGEVAIMNLADALDSYIPTPERAVDGTFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G++KVG+E+EIVGI+ATQKTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VLC
 Sbjct: 237 GIIKVGEIEIVGIKATQKTTCTGVEMFRKLLDQGQAGDNVGILLRGTKREDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
 KPGSI FH F E+Y+LSK+EGRHTPFF NYRPQFY RTTDVTGSI LP+ EMVMPG
 Sbjct: 297 KPGSIKPHTHFTGEVYIILSKDEGGRHTPFFNNYRPQFYFRTTDVTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV ITV+LI+P+A+E G +FAIREGGRTVGAGV+ IIE
 Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q7M7F1 Translation elongation factor Tu (EC 3.6.1.48) [tufA] 396 AA
Q7M7F1_CHRVO [Chromobacterium violaceum]
align

Score = 573 bits (1477), Expect = e-162
 Identities = 286/399 (71%), Positives = 329/399 (81%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF RT PHVN+GTIGHV HGKTTL+AAI+ +LS K E KDY ID+AP+EK RG
 Sbjct: 1 MAKEKFERTKPHVNVTIGHVDHGKTTAAITIILSKKFGGEAKDYSQIDSAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+NIEYET RHYAHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITINTAHIEYETANRHAYHDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTP+ GSA ALE
 Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDAELLELVELEMVERLLSKYDFPGDDTPIVTGSARLALE 180

Query: 181 EAKAGNVGEWGE-KVLKLMAEVDSYIPTPERDTEKTLMPVEDVFSIAGRGTVVTGRIER 239
 G+ E GE + +L +DSYIPTPER +K FL+P+EDVFSI+GRGTVVTG+ER
 Sbjct: 181 ----GDQSEMGEPSIFRLADALDSYIPTPERAIDKPFLPIEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKG+E+EIVGI+T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL
 Sbjct: 237 GIVKVGEIEIVGLKDTVKTCTGVEMFRKLLDQGQAGDNVGILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
 KPG+ITPH KEE +YVLSK+EGRHTPFF NYRPQFY RTTDVTG+I+L EGVEMMPG
 Sbjct: 297 KPGTITPHTKFEASVYVLSKDEGGRHTPFFANYRPQFYFRTTDVTGAISLAEGVEMMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 DNV+I VELI+P+A+E G +FAIREGGRTVGAGVV+ II
 Sbjct: 357 DNVEIKVELIAPIAMEEGLRFAIREGGRTVGAGVVAKII 395

sp Q50306 Elongation factor Tu (EF-Tu) [tuf] [Bacillus
 EFTU_BACST stearothermophilus] 395
 AA
align

Score = 571 bits (1472), Expect = e-162
 Identities = 283/400 (70%), Positives = 327/400 (81%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAK KF RT PHVNIGTIGHV HGKTL+AAI+ VL+ +G AE K YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERTKPHVNIGTIGHVDHGKTLAAITVLAKQGKAEAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETEARHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+TVVFLNK S Y+FPGD+ P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPYIVVFLNKCDMVDEELLELVEMEVRDLLSEYDFPGDEVPIKGALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W EK+++IM VD YIPTP+R+ +K F+MP+EDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GDPKWEEKIELMNAVDEIPTPQREVDKPFMMPIEDVFSITGRGTATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQK-TTVTGEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +KVGD VEI+G+ K TTVTGEMFRK L++ EAGDN+G LLRG ++EVERG VL
 Sbjct: 236 TLKVGDPVEIIGLSDEPKATTVTGEMFRKLLDQAEAGDNIGALLRGVSRDEVERGQVLA 295

Query: 300 KPGSITPHKKFEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSITPH KF+ +YVL+KEEGGRHTPFT+NYRPQFY RTTDVTG ITLPEGVEMVMPG
 Sbjct: 296 KPGSITPHTKFKAQVYVLTKEEGGRHTPFFSNYRPQFYFRTTDVTGIITLPEGVEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 399
 DNV++TVELI+P+A+E GTKF+TREGGRTVGAG VS ITE
 Sbjct: 356 DNVEMTVELIAPIAIEEGTKFSIREGGRTVGAGSVSEIIIE 395

tr Q5L3Z9 Translation elongation factor Tu (EF-Tu) [tufA] 395
Q5L3Z9_GEOKA [Geobacillus
 kaustophilus] AA
align

Score = 570 bits (1470), Expect = e-161
 Identities = 282/400 (70%), Positives = 327/400 (81%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAK KF RT PHVNIGTIGHV HGKTL+AAI+ VL+ +G AE K YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERTKPHVNIGTIGHVDHGKTLAAITVLAKQGKAEAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITISTAHVEYETDARHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LLSRQVGVP+IVVFLNK S Y+FPGD+ P++ GSAL+ALE

Sbjct: 121 LLSRQVGVPYIVVFLNKCDMVDEELLEVEMEVRDLLSEYDFPGDEVPIKGALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
+W EK+++LM VD YIPTP+R+ +K F+MP+EDVFSI GRGTIV TGR+ERG

Sbjct: 181 -----GDPOEEKIILMNAVDEYIPTPQREVDKPFMMPIEDVFSITGRGTATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQK-TTVTGEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
+KVSD VEI+G+ K TTVTGEMFRK L++ EAGDN+G LRG ++EVERG VL

Sbjct: 236 TLKVGDPVEIIGLSDPKTTTGTGEMFRKLLDQAEAGDNIGALLRGVSDEVERGVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
KPGSITPH KF+ ++YVL+KEEGGRHTPFFTNYRPQFY RFTTDVTG KTLPEGVEMVMPG

Sbjct: 296 KPGSITPHTKFKAQVYVLTKEEGGRHTPFFSNYRPQFYFRTTDVTGIITLPEGVEMVMPG 355

Query: 360 DNVKITVELISPVAELGTKFAIREGGRTVGAGVVSNIIE 399
DNV++TVELI+P+A+E GTKF+IREGGRTVGAG VS IIE

Sbjct: 356 DNVEMTVELIAPIAIEEGTKFSIREGGRTVGAGSVSEIIIE 395

tr Q5P334 Elongation factor Tu [tufB] [Azoarcus sp. (strain EbN1)] 396 AA
Q5P334_AZOSE
align

Score = 569 bits (1466), Expect = e-161
Identities = 286/400 (71%), Positives = 326/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTPHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
MAK KF RT PHVN+CTIGHV HGKTTL+AAI+ +LS K E K YD ID AP+EK RG
Sbjct: 1 MAKGKFERTKPHVNVTGIGHVHDHGKTTAAITTLISKKFGGEAKAYDQIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI T+H+EYET RNYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
Sbjct: 61 ITINTAHVEYETANRHAYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LL+RQVGVP+I+VFLNK S Y+FPGD+ P+ GSAL+ALE

Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDEELLEVEMEVRELLSKYDFPGDDVPIIKGALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIER 239
G+ + GE + +AE +DSYIPTPER ++ FL+F+EDVFSI+GRGTIVTGR+ER
Sbjct: 181 -----GDQSDIGEPAIFRLAELDSYIPTPERAIDRPFLPIEDVFSISGRGTVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
G+VKVG+EVVIVGSI+AE KTT TGEMFRK L++G+AGDNVGVLLRGTK+E+VERG VLC
Sbjct: 237 GIVKVGEEVEIVGIKATVKTCTGEMFRKLLDQGQAGDNVGVLLRGTKREDVERGVLC 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
KPGSITPH KF E+YVLSKEEGGRHTPFFTNYRPQFY RFTTDVTGSI LPEG EMVMPG
Sbjct: 297 KPGSIKPHTHFTGEVYVLSKEEGGRHTPFFNNYRPQFYFRTTDVTGSIELPEGTEMVMPG 356

Query: 360 DNVKITVELISPVAELGTKFAIREGGRTVGAGVVSNIIE 399
DNV ITV+I++P+A+E G +FAIREGGRTVGAGVV+ IIE

Sbjct: 357 DNVSITVKLMAPIAMEEGLRFAIREGGRTVGAGVVAKII 396

sp Q8R7T8 Elongation factor Tu-B (EF-Tu-B) [tufB] 400
EFTU2 THETN [Thermoanaerobacter AA
tengcongensis] align

Score = 568 bits (1464), Expect = e-161
Identities = 284/400 (71%), Positives = 323/400 (80%), Gaps = 1/400 (0%)

Query: 1 MAKEKFNRTPHVNIGTIGHVYHGKTLSSAIAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
MAK+KF RT PHVN+GTIGHV HGKTL+AAI+ +LS GLA+ K YD ID AP+EK RG
Sbjct: 1 MAKOKFERTKPHVNVTIGHVDHGKTLTAITLILSKAGLАОАКГҮДЕІДКАПЕЕКARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAI LVVSAADGPMPQTREHI 120
ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAI LVVSAADGPMPQTREHI
Sbjct: 61 ITINTTHVEYETAKRHAYVDCPGHADYVKNMITGAAQMDGAI LVVSAADGPMPQTREHI 120

Query: 121 LLSRQGVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 EK+PQGVGP+IVVFLNK + YRFPGD+TPIV GSAL+ALE
 Sbjct: 121 LLARQGVGVPHIVVFLNKADMVDDPELIELVEMEVBDLJNOYEFPGDETRIVVGSAKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
+W K+ +LM VD YIPTPERD +K FLMPVEDVFSI GRGTIV TGR+ERG
Sbjct: 181 CGCGKGRECOWCWKIWEIMDVVDEYIPTPERDIDKPELMPVEDVFSITGRGTVATGRVERG 240

Query: 241 VVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLC 299
 VKVGDEVEI+G+ +KT VTGVEMFRK L++ +AGDN+GVLLRG +K+EVERG VL
 Sbjct: 241 KVKGDEVEIIGITTESPKTVTGVEMFRKTLDEAQACDNLGYLRCIOKDEVERGVL 300

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMG 359
KPG+T PR KFE ++YVL+KEEGGRHTPFF VRPQFY RTTDVTG+I LPEGVEMVMG
Sbjct: 301 KPGTICKHTEKEEAOVXVLTKEEGCRHTPENCYRPOFYRTTDVTGCTIOLPEGVEMVMG 360

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
U+V + VELI+P+A+E G KFAIREGGRTVGAGVVS IIE
Sbjct: 361 DHVTLLRVELITPIAMEGLIKFAIREGGRTVGAGVVSATIE 400

sp Q8R603 Elongation factor Tu (EF-Tu) [tuf] [Fusobacterium 394
 EFTU_FUSNN nucleatum (subsp. AA
 nucleatum)] align

Score = 568 bits (1463), Expect = e-160
Identities = 280/397 (70%), Positives = 324/397 (81%), Gaps = 5/397 (1%)

Query: 1 MAKEKFNRTNPNVNIGTIGHVYHGKTLSSAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
MAKEKF+ R+ PRVNIGTIGHV HGKTT +AAIG VLS KG A D+G TD AP+EKERG
Sbjct: 1 MAKEKYERSKPHVNIGTIGHVDHGKTTTAISKVLSDKGWASKVDEOIDAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAQMDGAILVVSAADGPMPQTREHI 120
ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAQMDGAILVVSAADGPMPQTREHI
Sbjct: 61 ITINTAHLEYETEKRHYAHVDCPGHADYVKNMITGAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LJSROVGVPHIVFLNKXXXXXXXXXXXXXXXXXXXX SAYEEFPDDTRIVAGSAI PALE 180

LLSRQVGVP+IVV+LNK + Y FPGDD P++ GS+L AL
 Sbjct: 121 LLSRQVGVPYIVVYLNKSDMVEDEELLELVEMEVRELLTEYGFPGDDIPVIRGSSLGALN 180

 Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 + W EK+L+LM VD+YIPTPER + FIMP+EDVF+I GRGTVVTGR+ERG
 Sbjct: 181 GEE----KWVEKILELMEAVDNYIPTPERAVDQFPLMPIEDVFTITGRGTVVTGRVERG 235

 Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+KVG+E+EIVGI+ T KTT TGVEMFRK L++G+AGDN+GVLLP.GTKKEEVERG VL K
 Sbjct: 236 VIKVGEIEIVGIKPTTCTGVEMFRKLLDQGQAGDNIGVLLRGTKKEEVERGQVLAK 295

 Query: 301 PGSIIPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PH F+ E+YVIL+K+EGGRHTPFFT YRPQFY RTTD+TG++TLP+GEMVMPGD
 Sbjct: 296 PGSIHPTNFKGEVYVLTKEGGRHTPFFTGYRPQFYFRTTDITGAVTLPDGVEMVMPGD 355

 Query: 361 NVKITVELISPVALELGKFAIREGGRTVGAGVVNSI 397
 N+ +TVELT P+A+E G +FAIREGGRTV +GVVS I
 Sbjct: 356 NITMTVELIHPPIAMEQGLRFAIREGGRTVASGVVSEI 392

tr Q63PZ6 Elongation factor Tu [tufA1] [Burkholderia pseudomallei] 396 AA
Q63PZ6_BURPS (Pseudomonas pseudomallei)
align

 Score = 568 bits (1463), Expect = e-160
 Identities = 287/400 (71%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

 Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF KT PHVN+GTIGHV HGKTL+AAI+ VLS K E K YD ID AP+EK RG
 Sbjct: 1 MAKEKFERTKPHVNVTIGHVDHGKTTAAIATVLSAKFGGEAKKYDEIDAPEEKARG 60

 Query: 61 ITIATSHIEYETETRHAYHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI, T+HIEYET RHYHVDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITINTAHIEYETANRHAYHVDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

 Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTP+ GSA ALE
 Sbjct: 121 LLARQVGVPYIIIVFLNKCDMVDDAELLELVEMEVRELLSKYDFPGDDTPIIKGSAKLALE 180

 Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE + +A+ +D+YIPTPER + FIMP+EDVF+I GRGTVVTGR+ERG
 Sbjct: 181 ----GDKGELGEVAIMNLADALDTIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRVER 236

 Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 GV+KVG+E+EIVGI+AT KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL
 Sbjct: 237 GVIKVGEIEIVGIKATAKTTCTGVEMFRKLLDQGQAGDNVGILLRGTKREDVERGQVLA 296

 Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 359
 KPGSITPH F E+YVLSK+EGGRHTPFFT NYRPQFY RTTDVTGSI LP+ EMVMPGD
 Sbjct: 297 KPGSITPHFTAEVYVLSKDEGGRHTPFFNNYRPQFYFRTTDVTGSIELPKDKEMVMPGD 356

 Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVNSIIE 399
 DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE
 Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q62GK3 Translation elongation factor Tu [tuf-1] [Burkholderia 396
Q62GK3_BURMA mallei AA
(Pseudomonas mallei)

Score = 568 bits (1463), Expect = e-160
 Identities = 287/400 (71%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLSSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K S K YD ID AP+EK RG
 Sbjct: 1 MAKEKFERTKPHVNVTIGHVDHGKTLAAIATVLSAKFGGEAKKYDEIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+HIEYET RHYAHVDCPGHADYVNMITGAAQMDGAILVV SAADGPMPQTREHI
 Sbjct: 61 ITINTAHIEYETANRHAYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTP+ GSA ALE
 Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDAELLELVEMEVRELLSKYDFPGDDTPIIKGSAKLALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE +I+D+YIPTPER + FLMPVEDVFSI+GRGTVVTGR+ER
 Sbjct: 181 ----GDKGELGEVAIMNLADALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLC 299
 GV+KVG+E+E+IVGI+AT KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL
 Sbjct: 237 GVIKVGEIEIVGIKATAKTTCTGVEMFRKLDQGQAGDNVGILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
 KPGSITPH F E+YVLSK+EGGRHTPFT NYRPQFY RTPDVTGSI LP+ EMVMPG
 Sbjct: 297 KPGSITPTHFTAEVYVLSKDEGGRHTPFFNNYRPQFYFRTTDVTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIE 399
 DNV IIV+LT+P+A+E G +FALFEGGRHTVGAGVV+ IIE
 Sbjct: 357 DNVSITVKLIAPIAMEEGLRAIREGGRTVGAGVVAKIIE 396

sp P42481 Elongation factor Tu (EF-Tu) [tuf] [Thiobacillus cuprinus] 396 AA
EFTU_THICU align

Score = 567 bits (1462), Expect = e-160
 Identities = 285/400 (71%), Positives = 324/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLSSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K S K YD ID AP+EK RG
 Sbjct: 1 MAKSKFERTKPHVNVTIGHVDHGKTLAAITTFLSSKGGEAKAYDQIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+HIEYET RHYAHVDCPGHADYVNMITGAAQMDGAILVV SAADGPMPQTREHI
 Sbjct: 61 ITINTAHIEYETANRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTP+ GSA ALE
 Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDAELLELVEMEVRELLSKYDFPGDDTPIIKGSAKLALE 180

Query: 181 EAKAGNVGEWGE-KVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE +IKL +D+YIPTPER + FLMPVEDVFSI+GRGTVVTGR+ER

Sbjct: 181 ----GDKGELGEA**I**LKLA**E**ALDTY**I**PTPERAVDGAFLMPVEDVFSISGRGTVVGRVER 236

Query: 240 GVVKGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
G++KVG+E+EIVG++ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+EEVERG VLC

Sbjct: 237 GI**I**KVGE**E**E**I**EIVGLKPTLKTTCTGVEMFRKLLD**Q**GQAGDNVGILLRGTKREEVERGQVLC 296

Query: 300 KPGSITPHKKFEE**E**IYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVPG 359
KPGSI PH F E+YVLSK+EGGRHTPF NYRPQFY RTTDVTG+I LP+ EMVPG

Sbjct: 297 KPGSIKPHTHFTA**E**VYVLSKDEGGRHTPFFNNYRPQFYFRTTDVTGAIELPKDKEMVPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 399
DNV ITP+LI+P+A+E G +FAIREGGRTVGAGVV+ ITI

Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKII 396

sp P48864 Elongation factor Tu (EF-Tu) [tuf] [Neisseria gonorrhoeae] 394 AA
EFTU_NEIGO

align

Score = 567 bits (1462), Expect = e-160
Identities = 280/398 (70%), Positives = 327/398 (81%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQE**K**ERG 60
MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K K YD TDNAP+EK RG
Sbjct: 1 MAKEKFERSKPHVNVGTIGHVDHGKTTLAA**L**TTILAKKFGGA**A**KAYD**Q**IDNAPEEKARG 60

Query: 61 ITIATSHIEYE**T**ETRHYAHVDCPGHADYVKNM**I**ITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI TSH+EYE**T**ETRHYAHVDCPGHADYVKNM**I**ITGAAQMDGAILVV SAADGPMPQTREHI
Sbjct: 61 ITINTSHVEYE**T**ETRHYAHVDCPGHADYVKNM**I**ITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALALE 180
LL+PQVGVP+I+VF+NK S+Y+FPGDD PIV GSAL+A**L**E
Sbjct: 121 LLARQVGVPYIIVFMNKCDMVDDAELFQLVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVGRIERG 240
A + EK+ +L +D YIPTPER +K FL+P+EDVFSI+GRGTVVGR+ERG
Sbjct: 181 GDAA----YE**E**KIFELATALDRYIPTPERAVDKPFLLPIEDVFSISGRGTVVGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 300
++ VGDE+EIVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VLC
Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLD**E**QAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEE**E**IYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVPGD 360
G+ITPH KF+ E+YVLSKEEGG HTFFF NYRPQFY RTTDVTG+ITL +GVEMVPG+
Sbjct: 296 RGTITPHTKFKAEVYVLSKEEGGPHTPFFANYRPQFYFRTTDVTGTITLEKGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
NV ITPVELI+P+A+E G +FAIREGGRTVGAGVV+ +I
Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSSVI 393

sp Q8R7V2 Elongation factor Tu-A (EF-Tu-A) [tufA]
EFTU1_THETN [Thermoanaerobacter tengcongensis]

400
AA
align

Score = 567 bits (1462), Expect = e-160
 Identities = 283/400 (70%), Positives = 323/400 (80%), Gaps = 1/400 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAK+KF R PHVN+GTIGNV HGKTTL+AAI+ VLS GLA+ K YD ID AP+EK RG
 Sbjct: 1 MAKQKFERTKPHVNVTGIGHVDHGKTLTAITLILSKAGLAQAKGYDEIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+H+EYET RHYAHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTTHVEYETAKRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+IVVFLNK + YFPGDDTPIV GSAL+ALE
 Sbjct: 121 LLARQVGVPYIVVFLNKADMVDDPELIELVEMEVRDLLNQYEFPGDDTPIVVGALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W K+ +LM VD YTPPTPERD +K FLMPVEDVFE+I GRGTIV TGR+ERG
 Sbjct: 181 CGCGKRECQWCGKIWEMLDVDEYIPTPERDIDKPFLMPVEDVFTITGRGTVATGRVERG 240

Query: 241 VVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLC 299
 VKVGDXVRL+G+ +K+ VTCGVEMFRK L++ +AGDN+GVLLRG +++EVERG VL
 Sbjct: 241 KVKGDEVEIIGLTTESRKTVTGVEMFRKTLDEAQAGDNIGVLLRGQIQRDEVERGQVLA 300

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPG+I PH KFE ++YVL+KEEGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPG
 Sbjct: 301 KPGTIKPHTKFEAQVYVLTKEEGGRHTPFFNGYRPQFYFRTTDVTGTIQLPEGVEMVMPG 360

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIE 399
 D+V + VELI+F+A+E G KFAIREGGRTVGAGVVS ITE
 Sbjct: 361 DHVTLRVELITPIAMEEGLKFAIREGGRTVGAGVVSIIIE 400

tr Q83ES6 Translation elongation factor Tu [tuf-2] [Coxiella 397
Q83ES6_COXBU burnetii] AA align

Score = 567 bits (1462), Expect = e-160
 Identities = 281/400 (70%), Positives = 333/400 (83%), Gaps = 4/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 M+KEKF R PHVN+GTIGNV HGKTTL+AAI+ VLS K E K +D IDNAF+E+ RG
 Sbjct: 1 MSKEKFVREKPHVNVTGIGHVDHGKTLTAALTKVLSEKYGGKAFDQIDNAPEERARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITIATSH+EY+++ RHYAHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITIATSHVEYQSDKRHYAHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 +L++RQVGVP+IVV+LNK +Y+FPGD+TPT+ GSAL+ALE
 Sbjct: 121 VLAKQVGVPNIVVYLNKADMVDDKELLELVEMEVRDLLNSYDFPGDETPIIVVGALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 K+ VGE +K+ +D+Y P PER +K FLMP+EDVFSI+GRGTIVVTGR+ERG
 Sbjct: 181 GDKS-EVGE--PSIILVETMDTYFPQPERAIDKPFLMPIEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLC 300

++KVGDE+EIYGT+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+EEVERG VI K
 Sbjct: 238 IIKVGDEIEIVGIKDTTCTGVEMFRKLLDEGQAGDNVGILLRGTKKEEVERGQVLAK 297

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGS-ITLPEGVEMVMPG 359
 PGSITPHKKF+ EIYVLSKEEGGRHTPFFT YRPQFY RPTTDVTGS ++LPEG+EMVMPG
 Sbjct: 298 PGSITPHKKFEAEIYVLSKEEGGRHTPFLQGYRPQFYFRTTDVTGQLLSPEGIEMVMPG 357

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNVK+TVELI+FVA++ G +FA+REGGRTVGAGVV+ TIE
 Sbjct: 358 DNVKVTVELIAPVAMDEGLRAVREGGRTVGAGVVTKIIE 397

tr Q7P364 Protein translation elongation factor Tu (EF-TU) 394
Q7P364_FUSNV [FNV2036] AA
 [Fusobacterium nucleatum subsp. vincentii ATCC 49256] align

Score = 567 bits (1462), Expect = e-160
 Identities = 279/399 (69%), Positives = 326/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEK+ R+ PHVNIGTIGHV HGKTT +AALS VLS KGLA D+D ID AP+EKERG
 Sbjct: 1 MAKEKYERSKPHVNIGTIGHVDHGKTTAAISKVLSDKGLASKVDFDQIDAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+HTEYET RHYAHVDCPGHADYVENMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTAHIEYETANRHAYHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALALE 180
 LLSRQVGV+I+V+LNK + Y FFGD+ P++ GS+L AL
 Sbjct: 121 LLSRQVGVPIIIVYLNKADMVDEELLELVEMEVRELLTEYFGPGDEIPVIRGSSLGALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 + +W EK++ IM VDSYIPTPER ++ FLMP+EDV+I GRGTVVTGR+ERG
 Sbjct: 181 GEE----KWIKEKIMELMDAVDSYIPTPERAIDQPFMLPIEDVFTITGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+KVG+E+ETVGI+ T KTT TGVEMFRK L++G+AGDN+GVLLRGTKKEEVERG VI K
 Sbjct: 236 VIKVGEIEIVGIKPTTCTGVEMFRKLLDQGQAGDNIGVLLRGTKKEEVERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPHKKF+ EIYVLSKEEGGRHTPFFT YRPQFY RPTTDVTGS ++LPEG+EMVMPGD
 Sbjct: 296 PGSIHPHTNFKGEVYVLTKEDEGGRHTPFFTGYRPQFYFRTTDITGAVTLPDGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+ +TVELI F+A+E G +FAIREGGRTV +GVVS II+
 Sbjct: 356 NITMTVELIHIPIAEQGLRFAIREGGRTVASGVVSEIIK 394

tr Q7TTF9 Elongation factor tu, EF-Tu [tufA] [Haemophilus ducreyi] 394' AA
Q7TTF9_HAEDU
 align

Score = 567 bits (1461), Expect = e-160
 Identities = 279/399 (69%), Positives = 323/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 M+KEKF RT PHVN+G+TIGHV HGKTTL+AAI+ VL+ + +D LDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVTGIGHVDHGKTTLAATTVLAKHFGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EY+TETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVATDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+AI
 Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDEELLELVEVEMEVRELLSQQYDFPGDDTPIVRGSALQALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 V EW EK+++L +DSYIF PER +K FL+P+EDVFSI+GRGTVTGR+ERG
 Sbjct: 181 -----GVPEWEEKIIELAQHLDSYIPEPERAIDKPFLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++K G+EVEIVGI+ T KTTVTGVEMFRK L++G AG+NVG LRGTK+EE+ERG VL K
 Sbjct: 236 IIKSGEEEIVGIKETTKTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PG+ITPHI FS E+YVLSKEEGGRHTPFFT YRPQFY RTPDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGТИPHDFESEVYVLSKEEGGRHTPKGYRPQFYFRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+K+TV LI F+A++ G +FAIREGGRTVGAGVV+ II+
 Sbjct: 356 NIKMTVSLIHIPIAMDEGLRFAIREGGRTVGAGVVAKIIK 394

sp <u>Q99QMO</u>	Elongation factor Tu (EF-Tu) [tufA] [Caulobacter	396
EFTU_CAUCR	crescentus]	AA
		<u>align</u>

Score = 566 bits (1460), Expect = e-160
 Identities = 285/399 (71%), Positives = 323/399 (80%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF RT FA NIGTIGHV HGKTTL+AAI+ L+ G A K YD TD AP+EK RG
 Sbjct: 1 MAKEKFERTKPHCNIGTIGHVDHGKTTLAITMTLAKSGGATAKKYDEIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+H+EYET RHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTAHVEYETANRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP +VVF+NK S+Y+FPGDD PI GSAL A+E
 Sbjct: 121 LLARQVGVPALVVFMNKCDMVDEELLELVEVEMEVRELLSSYQFPGDDIPITKGSALAAVE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 + +GE EK+L+LMA VD+YIP PER + FLMPVEDVFSI+GRGTVTGR+ERG
 Sbjct: 181 -GRDPQIGE--EKILELMASVDAYIPQPERPVDMPLMPVEDVFSISGRGTVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VXVG+EVEIVGTR QKTT TGEMFRK L+G+AGDNVGVLLRGTK+EE+ERG VLCK
 Sbjct: 238 IVKVGEEEIVGIRPVQKTTCTGVEMFRKLLDQGQAGDNVGVLLRGTKREDVERGQVLCK 297

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH KF E Y+L+KEEGGRHTPFFTNYRPQFY RTTDVTG I L EGVEM+MPGD
 Sbjct: 298 PGSITPHTKFVAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDVTGIIKLREGVEMIMPGD 357

Query: 361 NVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIE 399
 N ++ VELI+P+A+E +FAIREGGRTVGAGVV+ I+E
 Sbjct: 358 NAELDVELITPIAMEEKLRFAIREGGRTVGAGVVAKIVE 396

sp Q8Y422 Elongation factor Tu (EF-Tu) [tuf] [Listeria 395
 EFTU_LISMO monocytogenes] AA
align

Score = 566 bits (1459), Expect = e-160
 Identities = 277/398 (69%), Positives = 325/398 (81%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R+ PHVNIGTIGHV HGKTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG
 Sbjct: 1 MAKEKFDRSKPHVNIGTIGHVDHGKTLTAAITTVLAKKGYADAQAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+R+EY+T++RHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTRENT
 Sbjct: 61 ITISTAHVEYQTDSSRHYAHHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVVFNLKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NK + YEFPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQVGVPYIVVFMNKCDMVDEELLELVEMEIRDLTEYEFPGDDIPVIKSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIERG 240
 +W K+ +EM VDSYIPTPERDT+K T+MPVEDVFSIAGRGTVVTGRIERG
 Sbjct: 181 -----GEADWEAKIDEMLAEVDSYIPTPERDTDKPFMMPVEDVFSIAGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 VKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LLRG +E+++RG VL
 Sbjct: 236 QVKVGDEVEVIGIEEESKKVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIORGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSITPH F+ E YVL+KEEGGRHTPFFT NYRPQFY RTTDVTG +TLPEG EMVMPG
 Sbjct: 296 KPGSITPHTNFKAETYVLTKEEGGRHTPFFNNYRPQFYFRTTDVTGIVTLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSNI 397
 DN+--- VELI+P+A+E GTKF+IREGGRTVGAGVVSNI
 Sbjct: 356 DNIELAELIAPIAIEDGTKFSIREGGRTVGAGVVSNI 393

sp Q71WB9 Elongation factor Tu (EF-Tu) [tuf] [Listeria monocytogenes 395 AA
 EFTU_LISMF (serotype 4b / strain F2365)]
align

Score = 566 bits (1459), Expect = e-160
 Identities = 277/398 (69%), Positives = 325/398 (81%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R+ PHVNIGTIGHV HGKTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG
 Sbjct: 1 MAKEKFDRSKPHVNIGTIGHVDHGKTLTAAITTVLAKKGYADAQAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EY+T++RHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYQTDSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NK + YEFPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQVGVPYIVVFMNKCDMVDEELLELVEIMEIRDLLEYEFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEVKLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W K+ +LM VDSYIPTPERDT+K F+MPVEDVFSI GRGTIV TGR+ERG
 Sbjct: 181 -----GEADWEAKIDELMEAVDSYIPTPERDTDKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLRLGKKEEVERGMVLC 299
 VKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LIRG +E+++RG VL
 Sbjct: 236 QVKVGDEVEVIGIEEESKKVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIORGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSITPHM F+ E YVL+KEEGGRHTPFFTNYRPQFY RTTDVFG +TPEG EMVMPG
 Sbjct: 296 KPGSITPHTNFKAETYVLTKEEGGRHTPFFNNYRPQFYFRTTDVTGIVTLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
 DN+++ VELI+P+A+E GTKF+IREGGRTVGAGVVSNI
 Sbjct: 356 DNIELAELIAPIAIEDGTKFSIREGGRTVGAGVVSNI 393

sp. Q92716 Elongation factor Tu (EF-Tu) [tuf] [Listeria innocua] 395 AA
EFTU_LISIN
align

Score = 566 bits (1459), Expect = e-160
 Identities = 277/398 (69%), Positives = 324/398 (80%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG
 Sbjct: 1 MAKEKFDRSKPHVNIGTIGHVDHGKTTLAAITVLAKKGFADAQAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EY+T+ RHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYQTDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NK + YEFPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQVGVPYIVVFMNKCDMVDEELLELVEIMEIRDLLEYEFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEVKLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W K+ +LM VDSYIPTPERDT+K F+MPVEDVFSI GRGTIV TGR+ERG
 Sbjct: 181 -----GEADWEAKIDELMEAVDSYIPTPERDTDKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLRLGKKEEVERGMVLC 299
 VKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LIRG +E+++RG VL
 Sbjct: 236 QVKVGDEVEVIGIEEESKKVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIORGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSITPHM F+ E YVL+KEEGGRHTPFFTNYRPQFY RTTDVFG +TPEG EMVMPG
 Sbjct: 296 KPGSITPHTNFKAETYVLTKEEGGRHTPFFNNYRPQFYFRTTDVTGIVTLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
 DN+--+ VELI+P+A+E GTKF+IREGGRTVGAGVVSNI
 Sbjct: 356 DNIELAELIAPIAIEDGTKFSIREGGRTVGAGVVSNI 393

tr Q81ZS3 GTPases-translation elongation factors and sulfate 396
Q81ZS3_NITEU adenylate AA
 transferase subunit 1 (EC 3.6.1.48) [tuf2] [Nitrosomonas align europaea]

Score = 565 bits (1457), Expect = e-160
 Identities = 280/399 (70%), Positives = 324/399 (81%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKEARG 60
 MAK KF R PHVN+GTTGRV HGKTLA+AAI+ VL+ K E K YD TD+AP+E+ RG
 Sbjct: 1 MAKSKFERVKPHVNVTIGHVDHGKTLAAITILTKKFGGEAKSYDQIDSAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTSHVEYETDKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLARQVGVPYIIVFMNKADMVDDAELLELVEIMEIRELLSNYDFPGDDTPIIIGSALKALE 180
 LL+RQVGVP+I+VF+NK S Y+FPGDDTP+ GSAL+ALE
 Sbjct: 121 LLARQVGVPYIIVFMNKADMVDDAELLELVEIMEIRELLSNYDFPGDDTPIIIGSALKALE 180

Query: 181 EAKAGNVGEWGEVKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIERG 240
 K+ ++GE +LKL +DSYIP PER + F+MPVEDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 GDKS-DIGE--AAILKLAEALDSYIPEPERAIDGAFIMPVEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLGKKEEVERGMVLCK 300
 +VKVGDE+EIVG++ T KT TGVEMFRK L+G+AGDNVG+LLRGK+EEVERG VL K
 Sbjct: 238 IVKVGDEIEIVGLKPTIKTVCTGVEMFRKLLDQGQAGDNVGILLRGKKEEVERGQVLAK 297

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PW KF EIVVLSKEEGGRHTPFF YRPQFY RTTDVTGSI LP GVERMVMMPGD
 Sbjct: 298 PGSILPHTKFTAEIYVLSKEEGGRHTPFAGYRPQFYRTTDVTGSIELPAGVEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+ +TV LI+P+A++ G +FAIREGGRTVGACVV+ +TE
 Sbjct: 358 NISVTVNLIAPIAMDEGLRFAIREGGRTVGAGVVAKIE 396

sp P57939 Elongation factor Tu-A (EF-Tu-A) [tufA] [Pasteurella 394
EFTU1_PASMU multocida] AA
align

Score = 565 bits (1456), Expect = e-160
 Identities = 277/399 (69%), Positives = 323/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKEARG 60
 M+KEKF RT PHVN+GTTGHV HGKTLA+AAI+ VL+ + +D IDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVTIGHVDHGKTLAAITVLAHYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVATDGPMPQTREHI 120

Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALALE 180
 LL RQGVGP+i+vflnk S Y+FPGDDTPIVAGSALALE
 Sbjct: 121 LLGRQGVVPYIIVFLNKCDMVDEELLELVEVRELLSQYDFPGDDTPIVRGSAQALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLMPVEDVFSIAGRGTVTGRIERG 240
 V EW EK+L+L +D+YIP PER ++ FL+P+EDVFSI+GRGTVTGR+ERG
 Sbjct: 181 -----GVAEWEKILELANHLDTYIPEPORAIDQPFLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +++ G+EVETVGI+AT KTTVTGVEMFRK L++G AG+NVG LLRGTK+EE+ERG VL K
 Sbjct: 236 IIRTGEEVEIVGIKATTKTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH FE E+YVLSKEEGGRHTPFFT YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPKGYRPQFYRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+K+TV LI P+A++ G +FATREGGRTVGAGVVS+ TT+
 Sbjct: 356 NIKMTVSLIHPIMDQGLRFAIREGGRTVGAGVVAKIIK 394

tr Q65QG6 TufB protein [tufB] [Mannheimia succiniciproducens] 394
Q65QG6_MANS (strain AA
MBEL55E) align

Score = 565 bits (1455), Expect = e-160
 Identities = 276/399 (69%), Positives = 322/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTPHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 M+K+KF RT FHN+G+TIGHV H+G+T+AAI+ VLS + +D IDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHNVNGTIGHVDHGKTTAAITVLSKHGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVATDGPMPQTREHI 120

Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALALE 180
 LL RQGVGP+i+vflnk S Y+FPGDDTPIVAGSALALE
 Sbjct: 121 LLGRQGVVPYIIVFLNKCDMVDEELLELVEVRELLSQYDFPGDDTPIVRGSAKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLMPVEDVFSIAGRGTVTGRIERG 240
 +W EK+L+L +D+YIP PER ++ FL+P+EDVFSI+GRGTVTGR+ERG
 Sbjct: 181 -----GEAQWEEKILEANALDTYIPEPERAIDQPFLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +++ G+EVETVGI+T KTTVTGVEMFRK L++G AG+NVG LLRGTK+EE+ERG VL K
 Sbjct: 236 IIRTGDEVEIVGIKETAKTTVTGVEMFRKLLDEGRAGENIGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH FE E+YVLSKEEGGRHTPFFT YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPKGYRPQFYRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

N+K+TV L I P+A++ G +FAIREGGRTVGAGVV+ T T+
 Sbjct: 356 NIKMTVSLIHPPIAMDQGLRFAIREGGRTVGAGVVAKIIK 394

tr Q8L160 Elongation factor Tu [tufA] [Myxococcus xanthus] 396 AA align
Q8L160_MYXXA

Score = 565 bits (1455), Expect = e-160
 Identities = 283/400 (70%), Positives = 324/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF R PHVNIGTIGHV HGKTF+L+AAI+ VL+ G A YD ID AP+E+ERG

Sbjct: 1 MAKEKFERNKPHVNIGTIGHVDHGKTSLTAAITKVLAKTGGATFLAYDLIDKAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+TSH+EY+T RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITISTSHVEYQTSNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+PQGVNP+IVVFLNK YEFFGDD PI+ GSAL+ALE

Sbjct: 121 LLARQGVVPYIVVFLNKVDMDDPELRELVEMEVRDLLKKYEFPGDDIPIIPGSALKALE 180

Query: 181 EAKAGNNGEWGEK-VLKLMMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ + GE +LKLM VDSYIPTP+R T+K FLMPVEDVFSI+GRGTV TGR+ER

Sbjct: 181 ----GDTSDIGEPAILKLMEAVDSYIPTPQRATDKPFLMPVEDVFSISGRGTVATGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+KVG+eve+VG+R TQKT VTGEMFRK L++G AGDN+G I+PG K+E++ERG VI

Sbjct: 237 GIIKVGEEVEVVGLRPTQKTVVTGEMFRKLLDQGMAGDNIGALVRGLKREDMERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
 KPGSITPH KF+ +IYVLSKEEGGRHTPFF YRPQFY RTTDVTGS+ LPE VEMVMPG

Sbjct: 297 KPGSITPHTKFKAQIYVLSKEEGGRHTPFFKGYRPQFYFRTTDVTGSVKLPENVEMMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIE 399
 DN+ I VELI+PVA+E +PA+REGGRRTVGAGVV+ IIE

Sbjct: 357 DNIAIEVELITPVAMEKELRFAVREGGRRTVGAGVVAEIE 396

tr Q5FTY1 Protein Translation Elongation Factor Tu (EF-TU) 396
Q5FTY1_GLUOX [GOX0382] AA
 [Gluconobacter oxydans (Gluconobacter suboxydans)] align

Score = 564 bits (1454), Expect = e-159
 Identities = 281/397 (70%), Positives = 326/397 (81%), Gaps = 3/397 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PH NIGTIGHV HGKTF+L+AAI+ VL+ G A YD ID AP+E+ RG

Sbjct: 1 MAKAKFERTKPHCNIGTIGHVDHGKTSLTAAITKVLAKTGGATYSAYDQIDKAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+K+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITISTAHVEYETADRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180

LL+RQVGVF +VVFLNK S+Y+FPGDD PIV GSAL IE
 Sbjct: 121 LLARQVGVPALVVFLNKVDQVDDPELLELVEMEVRELLSSYQFPGDDIPIVKGSALVTLE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 + +GE ++VL+LM +VD+YIP PER ++ FIMP+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 DGDP-SIGE--DRVLELMTQVDAYIPQPERPVDRPFLMPIEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK 300
 VV VGDEVEIVG++ T KTTVTGVEMFRK L++GEAGDN+G L+PGTK+E+VERG VL K
 Sbjct: 238 VVNVGDEVEIVGLKDTVKTTVTGVEMFRKLLDRGEAGDNIGALVRGRTKREDVERGQVLAK 297

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPHKKF+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDVTG +LPEG EMVMPGD
 Sbjct: 298 PGSITPHKKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDVTGVVTLPEGTEMVMPGD 357

Query: 361 NVKITVELISPVALELGKFAIREGGRTVGAGVVSSI 397
 NV + VELI+P+A++ G +FAIREGGRTVGAGVVSSI
 Sbjct: 358 NVAMDVELIAPIAMDEGLRFAIREGGRTVGAGVVSSI 394

sp Q8ETY4 Elongation factor Tu (EF-Tu) [tuf] [Oceanobacillus
 EFTU_OCEIH iheyensis] 395
 AA align

Score = 564 bits (1453), Expect = e-159
 Identities = 279/398 (70%), Positives = 322/398 (80%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF+R+ HVN+GT+GHV HGKTL+AAI+ VL+ G E + YD ID AP+E+ERG
 Sbjct: 1 MAKEKFDRSKSHVNVTGTLGHVDHGKTTLAATTVLAKHGGEARAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVF VVFLNK + Y+FPGDD P++ GSAL+ALE
 Sbjct: 121 LLSRNVGVPVFNLKTDMVDEELLEVEMEVRDLLTEYDFPGDDLPVIKGSAKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 V E+ E++L+IMA VD YIPTPERD EK F+MPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GVAEYEERILELMAAVDEYIPTPERDKEKPMMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK 299
 VVKVGDEVEI+G+ KTTVTGVEMFRK L+ EAGDN+G LIRG +E++ RG VL
 Sbjct: 236 EVKVGDEVEIIGLAEDASKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREDINRGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFY RTTDVTG I LPEG EMVMPG
 Sbjct: 296 KPGSITPHTNFKAEVYVLSKEEGGRHTPFFSNYRPQFYFRTTDVTGIELPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSSI 397
 DNV+TVELISP+P+A+G GT+F+IREGGRTVG+GVVS+I
 Sbjct: 356 DNIEMTVELISPIAIEDGTRFSIREGGRTVGSGVVSSI 393

tr Q605B0 Translation elongation factor Tu [tuf-2] [Methylococcus capsulatus] 396
Q605B0 AA
METCA align

Score = 563 bits (1452), Expect = e-159
 Identities = 279/400 (69%), Positives = 326/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLSSAISAVLSLKGLAEMKDYNIDNAPQEKE 60
 M+KEKF RT PHVN+GTIGHV HGKTTL+AA++ ++ K S K YD ID AP+E+ RG
 Sbjct: 1 MSKEKFTRTKPHNVNGTIGHVDHGKTLTAALTKCMAAKFGGEFKAYDQIDAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITIAT+H+EYE+ RHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITIATAHVEYESAARHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+IVVFLNK S Y+FPGDD PI+ GSAL+ALE
 Sbjct: 121 LLARQVGVPYIVVFLNKADMVDDPELLELVEMEVRELLSKYDFPGDDIPIIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ E G + + + + D YIP PER ++ FLMP+EDVFSI+GRGTVVTGR+ER
 Sbjct: 181 ----GDGSEIGVPAVEALVQALDDYIPEPERAIDRPFLMPIEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLC 299
 G+ +RKG+ +E+IVGIR T KTT TGVEMFRK L+ +G+AGDN+GVLLRGTK+E+VERG VL
 Sbjct: 237 GIKVGEIEIVGIRPTAKTTCTGVEMFRKLLDQQAGDNIGVLLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
 KPGSITPH F E IYVLSKEEGGRHTPFT YRPQFY RPTDVTG++TLPEGVEMMPG
 Sbjct: 297 KPGSITPHFEAEIYVLSKEEGGRHTPFFNGYRPQFYFRTTDVTGAVTLPEGVEMMPG 356

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSKIIE 399
 DNVKI V+L+P+A++ G +PA+REGGRTVGAGVV S IIE
 Sbjct: 357 DNVKIEVKLIAPIAMDEGLRAVREGGRTVGAGVVSKIIE 396

tr Q8EK70 Translation elongation factor Tu [tufA] [Shewanella oneidensis] 394
Q8EK70 AA
SHEON align

Score = 563 bits (1450), Expect = e-159
 Identities = 278/398 (69%), Positives = 320/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLSSAISAVLSLKGLAEMKDYNIDNAPQEKE 60
 MAK KE R+ PHVN+GTIGHV HGKTTL+AAIS VL+ S KD+ IDNAP+E+ERG
 Sbjct: 1 MAKAKFERSKPHNVNGTIGHVDHGKTLAAISHVLAKTYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHEY+T +RHYAHDVDCPGHADYVKNMITGAAQMDGAILVV++ DGMPQTREHI
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVASTDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPYIVFMNKCDMVDDAELLELVEMEVRELLSEYDFPGDDLPVIQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 EW K+L+I A +DSYIP PERD +K FLMP+EDVFSI+GRGTVVTGR+ERG

Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPERDIDKPFLMPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
+V+VGDEVEIVGIR T KTT TGVEMFK L++G AG+N G+LLRGTK+++VERG VL K

Sbjct: 236 IVRVGDEVEIVGIRTTKTTCTGVEMFRKLLDEGRAGENCGILLRGTKRDDVERGQVLSK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PGSI PH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGD

Sbjct: 296 PGSINPHTTFESEEVYVLSKEEGGRHTPKGYRPQFYFRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGKFAIREGGRTVGAGVVSNII 398
N+N+ V LI P+A++ G +FAIREGGRTVGAGVV+ II

Sbjct: 356 NIKMVVTLICPIAMDEGLRFAIREGGRTVGAGVVAKII 393

tr Q7TT91 Elongation factor Tu [tufA] [Bordetella pertussis] 396 AA
Q7TT91_BORPE align

Score = 563 bits (1450), Expect = e-159

Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
MAK KE RT PHVN+GTIGHV HGKTTL+AAL+ VLS K E + YD ID AP+EK RG

Sbjct: 1 MAKGKFERTKPHVNVTGIGHVDHGKTLTAAITVLSNKFGGEARGYDQIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI TSH+EYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITINTSHVEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALALE 180
LLSRQVGVP+I+VFLNK S Y+FPGDDTPIV GSA ALE

Sbjct: 121 LLSRQVGVPYIIVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIVKGSAKLALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
G+ GE GE+ +L L +D+YIPTPER + FLMPVEDVFSI+GRGTVVTGRIER

Sbjct: 181 ----GDKGELGEQAILS LAQALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
GVVKVG+E+EIVGI+ T KTT TGVEMFK L++G+AGDNVG+LLRGTK+E+VERG VL

Sbjct: 237 GVVKVGEEIEIVGIKPTVKTCTGVEMFRKLLDQGQAGDNVGILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
KFGSI PH F E+Y+LSKEEGGRHTPFF YRPQFY RTTDVTG+I LF EMV+PG

Sbjct: 297 KPGSINPHTDFTAEVYIILSKEEGGRHTPFFNGYRPQFYFRTTDVTGIDL PADKEMVLPG 356

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSNII 399

UNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+

Sbjct: 357 DNVSMTVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKII 396

tr Q79GC6 Elongation factor Tu [tuf] [Bordetella parapertussis] 396 AA
Q79GC6_BORPA align

Score = 563 bits (1450), Expect = e-159

Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEARG 60
MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E + YD ID AP+EK RG
Sbjct: 1 MAKGKFERTKPHVNVTIGHVDHGKTLAAITVLSNKFGGEARGYDQIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI TSH+EYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
Sbjct: 61 ITINTSHVEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
LLSRQVGVP+I+VFLNK S Y+FPGDDTPIV GSA ALE
Sbjct: 121 LLSRQVGVPYIIVFLNKADMVDDAELLELVEVRELLSKYDFPGDDTPIVKGSAKLALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
G+ GE GE+ +L L +D+YIPTPER + FLMPVEDVFSI+GRGTVVTGRIER
Sbjct: 181 ----GDKGELGEQAILS LAQALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLC 299
GVVKVG+E+EIVGI+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL
Sbjct: 237 GVVKVGEEIEIIVGIKPTVKTTCTGVEMFRKLDQGQAGDNVGILLRGTKREDVERGVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
KPGSI PH F E+Y+LSKEEGGRHTPFF YRPQFY RPPDTVG+I LP EMV+PG
Sbjct: 297 KPGSINPHTDFTAEVYIILSKEEGGRHTPFFNGYRPQFYFRTTDVTGTIDL PADKEMVLPG 356

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIE 399
DNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+
Sbjct: 357 DNVSMTVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKIIK 396

tr Q79G84 Elongation factor Tu [tuf] [Bordetella bronchiseptica] 396
Q79G84_BORBR (Alcaligenes AA
bronchisepticus)] align

Score = 563 bits (1450), Expect = e-159
Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKEARG 60
MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E + YD ID AP+EK RG
Sbjct: 1 MAKGKFERTKPHVNVTIGHVDHGKTLAAITVLSNKFGGEARGYDQIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI TSH+EYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
Sbjct: 61 ITINTSHVEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
LLSRQVGVP+I+VFLNK S Y+FPGDDTPIV GSA ALE
Sbjct: 121 LLSRQVGVPYIIVFLNKADMVDDAELLELVEVRELLSKYDFPGDDTPIVKGSAKLALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
G+ GE GE+ +L L +D+YIPTPER + FLMPVEDVFSI+GRGTVVTGRIER
Sbjct: 181 ----GDKGELGEQAILS LAQALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLC 299
GVVKVG+E+EIVGI+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL

Sbjct: 237 GVVKVGEEIEIVGIKPTVKTTCTGVEMFRKLLDQGQAGDNVGILLRGTKREDVERGVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
KPGSI PH F E+Y+LSKEEGGRHTPFF YRPQFY RTTDVTG+I LF EMV+PG

Sbjct: 297 KPGSINPHTDFTAEVYIILSKEEGGRHTPFFNGYRPQFYFRTTDVTGTIDLPADKEMVLPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

DNV +TV+L++P+A+E G +FAIREGGRTVGAGVVS II+

Sbjct: 357 DNVSMTVKLLAPIAMEEGLRFAIREGGRTVGAGVVAIIK 396

tr Q5GWR8 Elongation factor Tu [tufB] [Xanthomonas oryzae (pv. oryzae)] 396
AA align

Score = 563 bits (1450), Expect = e-159

Identities = 281/400 (70%), Positives = 327/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGKLAEMKDYNIDNAPQEKERG 60
MAK KF RT PHVN+GTIGHV HGKTTL+AA++ ++ E K YD ID AP+EK RG

Sbjct: 1 MAKAKFERTKPHVNVTIGHVDHGKTTAALTKIGAERFGGEFKAYDAIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

ITI+T+H+EYE+ +RHAYHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI

Sbjct: 61 ITISTAHVEYESPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALALE 180

LLSRQVGVPHIVVFLNK S Y+FPGDDTP+ GSA AL+

Sbjct: 121 LLSRQVGVPHIVVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIIHGSARLALD 180

Query: 181 EAKAGNVGEWG-EKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239

G+ E G +LKL+ +D++IP P RD ++ FLMPVEDVFSI+GRGTVVTGRIER

Sbjct: 181 ----GDQSEIGVPAILKLVDALDTFIPEPTRDVRPFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLC 299

G++KVGDE+EIVGIRATQKTTVTGVEMFRK L++G+AGDN G+LLRGTK+++VERG VLC

Sbjct: 237 GIIKVGDEIEIVGIRATQKTTVTGVEMFRKLLDQGQAGDNAGLLRGTKRDDVERGVLC 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359

KPGSI PH F E+YVLSK+EGGRHTPFF YRPQ Y RTTD+TG+I LPEGVEMMPG

Sbjct: 297 KPGSIKPTEFEAEVYVLSKDEGGRTPKGYRPQLYFRTTDITGAIDLPEGVEMMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

DNV+TV LI+PVA++ G +FAIREGGRTVGAGVVS II+

Sbjct: 357 DNVKMTVTLINPVAMDEGLRFAIREGGRTVGAGVVSIIK 396

sp P43926 Elongation factor Tu (EF-Tu) [tufA] [Haemophilus influenzae] 393
AA align

Score = 562 bits (1448), Expect = e-159

Identities = 275/398 (69%), Positives = 321/398 (80%), Gaps = 5/398 (1%)

Query: 2 AKEFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGKLAEMKDYNIDNAPQEKERGI 61

+KEKF RT PHVN+GTIGHV HGKPTL+AAI+ VL+ + +D IDNAP+EK RGT
 Sbjct: 1 SKEKFERTKPHVNVTGIGHVDHGKTLTAAITTVLAKHYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHIL 121
 TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHIL

Sbjct: 61 TINTSHVEYDTPTRHAYHVDCPGHADYVKNMITGAAQMDGAILVVAAATDGPMPQTREHIL 120

Query: 122 LSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
 L RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+AL

Sbjct: 121 LGRQVGVPYIIVFLNKCDMVDEELLELVEVEMEVRELLSQYDFPGDDTPIVRGSGALQALN- 179

Query: 182 AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERGV 241
 V EW EK+L+I +D+YIP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG+
 Sbjct: 180 ----GVAEWEKILELANHLDTYIPEPERAIDQPFLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
 ++ GDEVEIVGI+ T KPTVVTGVEMFRK L++G AG+N+G LLRGTK+EE+ERG VL KP
 Sbjct: 236 IRTGDEVEIVGIKDTAKTTVTGVEMFRKLLDEGRAGENIGALLRGTKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDN 361
 GSITPH FE E+YVLSK+EGGRHTPFF YRPQFY KPTDVTG+T LPEGVEMVMPGDN
 Sbjct: 296 GSITPHTDFESEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALEGTKFAIREGGRTVGAGVVSNIIE 399
 +K+TV LT P+A++ G +FAIREGGRTVGAGVV+ II+
 Sbjct: 356 IKMTVSLIHPIAMDQGLRFAIREGGRTVGAGVVAKIIK 393

sp P57966 Elongation factor Tu-B (EF-Tu-B) [tufB] [Pasteurella 394
 EFTU2_PASMU multocida] AA
align

Score = 561 bits (1447), Expect = e-159
 Identities = 275/399 (68%), Positives = 322/399 (79%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 M+KEKF RT PHVN+GTIGHV HGKPTL+AAI+ VL+ + +D IDNAP+EK RGT
 Sbjct: 1 MSKEKFERTKPHVNVTGIGHVDHGKTLTAAITTVLAKHYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI

Sbjct: 61 ITINTSHVEYDTPTRHAYHVDCPGHADYVKNMITGAAQMDGAILVVAAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 180
 LL RQ+GV +I+VFLNK S Y+FPGDDTPIV GSAL+AL

Sbjct: 121 LLGRQIGVAYIIVFLNKCDMVDEELLELVEVEMEVRELLSQYDFPGDDTPIVRGSGALQALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 V EW EK+L+I +D+YIP P+R ++ FL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 ----GVAEWEKILELANHLDTYIPEPQRAIDQPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +++ G+EVEIVGI+AT KTTVVTGVEMFRK L++G AG+N+G LLRGTK+EE+ERG VL K

Sbjct: 236 IIRTGEEVEIVGIKATTKTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

PGSITTPH FB E+YVLSKEEGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSITPHDFESEVVYVLSKEEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+K+TV LI P+A++ G +FAIREGGRTVGAGVVS+ LI+
 Sbjct: 356 NIKMTVSLIHIPIAMDQGLRFAIREGGRTVGAGVVAKIIK 394

tr Q65PA9 TufA (Elongation factor Tu) [tufA] [Bacillus 396
Q65PA9_BACLD licheniformis (strain AA
 DSM 13 / ATCC 14580)] align

Score = 561 bits (1447), Expect = e-159
 Identities = 281/401 (70%), Positives = 326/401 (81%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVLSLK-GLAEMKDYNIDNAPQEKER 59
 MAKEKF+R+ R NIIGTGRV HGKTTL+AAT+ VL K G YD ID AP+E+ER
 Sbjct: 1 MAKEKFDRSKSHANIGTIGHVDHGKTTLAAITVLHKSGKGTAMAYDQIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHAYVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH 119
 GITI+T+R+EYET+ RHAYVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH
 Sbjct: 61 GITISTAHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH 120

Query: 120 ILLSRQGVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179
 ILLSR VGV+IVVFLNK S YEFPGDD P++ GSAL+AL
 Sbjct: 121 ILLSRNVGVPYIVVFLNKCDMVDDEELLELVEMEVRDLLSEYEFPGDDVPVIKGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 E ++ EK+ +LMA VB YIPTPER+T+K F+MPVEDVFSI GRGTV TCR+ER
 Sbjct: 181 E-----GDAQYEKEKIFELMAAVDEYIPTPERETDKPFMMPVEDVFSITGRGTVATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298
 G VKVGDEVEI+G++ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EE++RG VL
 Sbjct: 236 GOVKVGDEVEIIGLQEEENKKTGTGVEMFRKLLDYAEAGDNI GALLRGVSREEIQRGQVL 295

Query: 299 CKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMP 358
 +PG+ITPHKKF+ E+YVLSKEEGGRHTPFFT+NYRPQFY RTTDVTG I LPEGVEMVMP
 Sbjct: 296 AQPGTITPHKKFKAEVYVLSKEEGGRHTPFFSNYRPQFYFRTTDVTGIIQLPEGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 GDN+---TVALIS +A+E GT+F+IREGGRTVG+GVVS+IIR
 Sbjct: 356 GDNIEMTVELISTIAIEDGTRFSIREGGRTVGSGVVSSIIE 396

sp P33169 Elongation factor Tu (EF-Tu) [tuf] [Shewanella 394
EFTU_SHEPU putrefaciens AA
 (Pseudomonas putrefaciens)] align

Score = 561 bits (1445), Expect = e-158
 Identities = 276/398 (69%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF R PHVN+GTIGHV HGKTTL+AATL VL+ S KD+ LDNAP+E+ERG
 Sbjct: 1 MAKAKFERIKPHVNVTIGHVDHGKTTLAAISHVLAKEYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHIEY+T +RHAYAHVDCPGHADYVKNMITGAAQMDGAILVV++ DGPMPQTREHI
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVASTDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVVFNLKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPFIIVFMNKCDMVDEELLELVELEMVERLLSEYDFPGDDLPVIQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 EW K+L+L A +DSYIP PERD +K FLMP+EDVFSI+GRGTVTGRIERG
 Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPQRDIDKPFLLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +V+VGDEVEIVG+RAT KTF TGVEMFRK L++G AG+N G+LLRGTK+++VERG VL K
 Sbjct: 236 IVRVGDEVEIVGVRATTKTTCTGVEMFRKLLDEGRAGENCGILLRGTKRDDVERGQVLAK 295

Query: 301 PGSITPHKKFEEEEEYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PH FE E+YVLSKEEGGRHTPFFT YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ TT
 Sbjct: 356 NIKMVVTLICPIAMDEGLRFAIREGGRTVGAGVVAKII 393

tr Q8EK81 Translation elongation factor Tu [tufB] [Shewanella 394
 Q8EK81_SHEON oneidensis] AA
align

Score = 561 bits (1445), Expect = e-158
 Identities = 277/397 (69%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF R+ PHVN+GTIGHV HGKTTL+AAIS VL+ E KD+ IDNAP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNVTGIGHVDHGKTTLAAISHVLAKTYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHIEY+T +RHAYAHVDCPGHADYVKNMITGAAQMDGAILVV++ DGPMPQTREHI
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVASTDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVVFNLKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPFIIVFMNKCDMVDDAELLELVELEMVERLLSEYDFPGDDLPVIQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 EW K+L+L A +DSYIP PERD +K FLMP+EDVFSI+GRGTVTGRIERG
 Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPERDIDKPFLMPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +V+VGDEVEIVGIR T KTF TGVEMFRK L++G AG+N G+LLRGTK+++VERG VL K
 Sbjct: 236 IVRVGDEVEIVGIRTTKTTCTGVEMFRKLLDEGRAGENCGILLRGTKRDDVERGQVLSK 295

Query: 301 PGSITPHKKFEEEEEYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PH FE E+YVLSKEEGGRHTPFFT YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ I
 Sbjct: 356 NIKMKVTLICPIAMDEGLRFAIREGGRTVGAGVVAKI 392

tr Q5NQ65 Translation elongation factor [ZMO0516] [Zymomonas] 397
Q5NQ65_ZYMMO mobilis AA align

Score = 561 bits (1445), Expect = e-158
 Identities = 283/400 (70%), Positives = 326/400 (80%), Gaps = 4/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGLAE-MKDYNIDNAPQEKER 59
 MAK KF R PH NIGTIGHV HGKTL+AAI+ VL+ G DY NID AP+E+ER
 Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTLAAITKVLAEGGGNTFVDYANIDKAPEERER 60

Query: 60 GITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH 119
 GITI+TSH+EYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH
 Sbjct: 61 GITISTSHVEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH 120

Query: 120 ILLSRQGVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRAL 179
 ILL+RQGVGP +VV+F+NN S+Y+FPGDD PIV GSAL AL
 Sbjct: 121 ILLARQGVGPALVVFMNKVDQVDDPELLELVEMEIRELLSSYDFPGDDIPIVKGSLAAL 180

Query: 180 EEAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 E+ K +G+ E +L LMA VD YIP PER +K+FLMP+EDVFST+GRGTVVTGR+E
 Sbjct: 181 ED-KNPEIGK--EAILSLMAAVDEYIPQPERPLDKSFLMPIEDVFSISGRGTVVTGRVET 237

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKVG+EVEIVG+R T+KTTVTGVEMFRK L++G+AGDN+G LLRG+ + EVERG VL
 Sbjct: 238 GIVKVGEEVEIVGLRDTKKTGTTVTGVEMFRKLLDQQAGDNIGALLRGARTATEVERGQVLA 297

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
 KPGSITPM +F+ E+YVLSK+EGGPHTFFF NYRFQFY RTTDTVG ITLFE VEMVMPG
 Sbjct: 298 KPGSITPHTEFKAEVYVLSKDEGGRHTPFFANYRPQFYRTTDVTGEITLPEDVEMMPG 357

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+ V+LI+P+A++ G +FAIREGGRTVGAGVV+II+
 Sbjct: 358 DNIAFGVKLIAPIAMDPLGLRFAIREGGRTVGAGVVSSIIE 397

sp Q8CQ81 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus] 394
EFTU_STAEP epidermidis AA align

Score = 560 bits (1444), Expect = e-158
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGLAE-MKDYNIDNAPQEKERG 60
 MAKEKF+R+ H NIGTIGHV HGKTL+AAI+ VL+ G + YD IDNAP+EKERG
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTLAAITVLAKNGDTVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+HIEY+T+ RHAYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTAHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVP +VFLNK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDEELLEVEMEVRLLLSEYDFPGDDPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 E+ +K+L LM VD YIPTPERD+K F+MPVEDVFSI GRGTIV TGR+ERG
 Sbjct: 181 -----GDAEYEQKILDLMQAVDDYIPTPERDSDKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGILLRGTKKEEVERGMVLCK 300
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL
 Sbjct: 236 QIKVGEEVEIIGMHETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVORGQVLAA 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH KF+ E+YVLSK+EGGRHTPFTNYRPQFY RTTDVTG + LPEG EMVMPGD
 Sbjct: 296 PGSITPHTKFKAEVYVLSKDEGGRHTPFTNYRPQFYRTTDVTGVVNLPAGEVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV+ +TVELI+P+A+E CT+F+IREGGRTVG+GVV+ T E
 Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIFE 394

sp P33167 Elongation factor Tu (EF-Tu) [tuf] [Burkholderia cepacia] 396 AA
EFTU_BURCE (*Pseudomonas cepacia*)

align

Score = 560 bits (1444), Expect = e-158
 Identities = 282/400 (70%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ K E K YD TD AP+EK RG
 Sbjct: 1 MAKGKFERTKPHVNNGTIGHVDHGKTTAAITVLTKKFGGEAKAYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+H+EYET RHYAHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITINTAHVEYETANRHAYHDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+I+VFLNK S Y+FPGDDTPIV CSA ALE
 Sbjct: 121 LLARQVGVPYIIVFLNKCDSDAELLEVEMEVRELLSKYDFPGDDTPIVKGSAKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE + +A+ +D+YIPTPER + FLMPVEDVFSI+GRGTIVTGR+ER
 Sbjct: 181 ----GDTGELGEVAIMSLADALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGILLRGTKKEEVERGMVLC 299
 G+VKVG+E+EIVGT+ T KTT VTGVEMFRK L++G+AGDNVG+LLRGTK+B+VGRG VL
 Sbjct: 237 GIVKVGEIEIVGIKPTVKTCTGVEMFRKLLDQGQAGDNVGILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSITPH F E+YVLSK+EGGRHTPFT NYRFQFY RTTDVTGSI LP+ EMVMPG
 Sbjct: 297 KPGSITPHTHFTAEVYVLSKDEGGRHTPFFNNYRPQFYRTTDVTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ I++
 Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKILD 396

tr Q5HRK4 Translation elongation factor Tu [tuf] [Staphylococcus 394
Q5HRK4_STAEQ epidermidis AA
(strain ATCC 35984 / RP62A)] align

Score = 560 bits (1444), Expect = e-158
Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + YD IDNAP+EKERG
Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLAAITVLAKNGDTVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI T+HTEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
Sbjct: 61 ITINTAHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LLSR VGVP +VVFLNK S Y+FPGDD P++AGSAL+ALE
Sbjct: 121 LLSRNVGVPAVVFLNKVDMVDEELLELVEVEMEVRDLLSEYDFPGDDPVIAAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
E+ +K+L IM VD YIPTPERD+ +K F+NPVEDVFSI GRGTIV TGR+ERG
Sbjct: 181 -----GDAEYEQKILDLMQAVDDYIPTPERDSDKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
+KVG+EVEI+G+ T KTTVTGVEMFRK E+ EAQDN+G LLRG +E+V+PG VI.
Sbjct: 236 QIKVGEVEIIGMHETS KTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVORGQVLAA 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PGSITPH KF+ E+YVLSK+EGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMPGD
Sbjct: 296 PGSITPHTKFKAEVYVLSKDEGGRHTPFFTNYRPQFYRTTDVTGVNLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIE 399
NV++TVELI+F+A+E GF+F+IREGGRTVG+GAV+ I E
Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIFE 394

sp Q9Z9L6 Elongation factor Tu (EF-Tu) [tuf] [Bacillus halodurans] 396 AA
EFTU_BACHD align

Score = 560 bits (1443), Expect = e-158
Identities = 279/399 (69%), Positives = 323/399 (80%), Gaps = 7/399 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLK-GLAEMKDYNIDNAPQEKER 59
MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G YD ID AP+E+ER
Sbjct: 1 MAKEKFDRSKTHANIGTIGHVDHGKTTLAAITVLAKRSGKGVAMAYDAIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHAYVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH 119
GITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREH
Sbjct: 61 GITISTAHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREH 120

Query: 120 ILLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179
ILLSRQVGVP++VVFLNK S Y+FPGDD P++ GSAL+AL

Sbjct: 121 ILLSRQVGVPYLVVFLNKCDMVDEELLELVEMEVRDILSEYDFPGDDVPVIRGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 E EW EK++ELMA VD YIPTPERDTEK F+MPVEDVFSI GRGTV TGR+ER

Sbjct: 181 E-----GDAEWEKKIELMAAVDDYIPTPERDTEKPMMMPVEDVFSITGRGTVATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVL 298
 G + VGDEVEI+G+ +KTVTGVEMFRK L+ EAGDN+G LLRG +EEV+RG VL

Sbjct: 236 GQLNNGDEVEIIGLEEEAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREEVQRGQVL 295

Query: 299 CKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMP 358
 KPG+ITPH F+ E+YVLSKEEGGRHTPFFTNYRPQFY RTTDVTG I LP+GVEMVMP

Sbjct: 296 AKPGTITPHTNFKAEVYVLSKEEGGRHTPFFSNYRPQFYFRTTDVTGIIQLPDGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGKFAIREGGRTVGAGVVSNI 397
 GDNV++TVELI+P+A+E GPKF+IREGGRTVGAGVVSNI

Sbjct: 356 GDNVEMTVELIAPIAIEEGTKFSIREGGRTVGAGVVASI 394

sp Q8NL22 Elongation factor Tu (EF-Tu) [tufA] [Xanthomonas 396
 EFTU_XANAC axonopodis (pv. AA
 citri)] align

Score = 560 bits (1442), Expect = e-158
 Identities = 279/400 (69%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTPHNIGTIGHVYHGKTLAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PNVN+GTIGHV HGKTLA+AA++ + + + E K YD ID AP+EK RG
 Sbjct: 1 MAKAKFERTKPHNVNGTIGHVDHGKTLTAALTIGAERFGGEFKAYDAIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+R+EYE+ TRHYAHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYESPTRHYAHDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIIVVFLNXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVPHIIVVFLNK S X+FPGDDTP+ GSA AL+
 Sbjct: 121 LLSRQVGVPHIIVVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIIHGSARLA 180

Query: 181 EAKAGNVGEWG-EKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ + G +LKL+ +DS+IP P RD ++ FLMPVEDVFSI+GRGTVVTGRIER
 Sbjct: 181 ----GDQSDIGVPAILKLVEALDSFIPEPTRDVDRPFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVL 299
 G++KVGDE+EIVGIR TQKTTVTGVEMFRK L++G+AGDN G+LLRGTK+++VERG VLC
 Sbjct: 237 GIIKVGDEIEIVGIRDTQKTTVTGVEMFRKLLDQGQAGDNAGLLLRGTRKDDVERGQVL 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSI PH +FE E+YVLSK+EGGRHTPFF YRPQFY RTTD+TG+ LPEGVEMVMPG
 Sbjct: 297 KPGSIKPHTEFEAEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDITGACQLPEGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIE 399
 DNVK+ V LI+PVA++ G +FAIREGGRTVGAGVV+ TI+
 Sbjct: 357 DNVKMVVTLINPVAMDEGLRFAIREGGRTVGAGVVAIIK 396

sp P33166 Elongation factor Tu (EF-Tu) (P-40) [tuf] [Bacillus
EFTU_BACSU subtilis] 396
AA
align

Score = 560 bits (1442), Expect = e-158
Identities = 282/401 (70%), Positives = 320/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRNPHVNIGTIGHVYHGKTLSSAISAVSLK-GLAEMKDYNIDNAPQEKER 59

MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL K G + YD ID AP+E+ER

Sbjct: 1 MAKEKFDRSKSHANIGTIGHVDHGKTLTAAITVLHKKSGKTAMAYDQIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH 119

GITI+T+H+EYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH

Sbjct: 61 GITISTAHVEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREH 120

Query: 120 ILLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRAL 179

ILL+S VGV+IVVFLNK S Y+FPGDD P+V GSAL+AL

Sbjct: 121 ILLSKNVGVPYIVVFLNKCDMVDEELLELVEMEVRLLLSEYDFPGDDVPVKGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIER 239

E EW K+ +LM VD YIPTPERDTEK F+MEVEDVFSI GRRTV TGR+EER

Sbjct: 181 E-----GDAEWEAKIFEELMDAVDEYIPTPERDTEKPFMMPVEDVFSITGRGTVATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVL 298

G VVVGDEVEI+G++ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EE+E+RG VE

Sbjct: 236 GQVKVGDEVEIIGLOQEENKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREEIQRGQVL 295

Query: 299 CKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMP 358

KPG+ITPH KF+ E+YVLSKEEGGRHTPFF+NYRPQFY RTTDVTG I LPEGVEMVMP

Sbjct: 296 AKPGTITPHSKFKAEVYVLSKEEGGRHTPFFSNYRPQFYFRTTDVTGIIHLPEGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIE 399

GDN ++ VELIS +A+E GT+F+IRREGGRTVG+GVVS I E

Sbjct: 356 GDNTEMNVELISTIAIEEGTRFSIREGGRTVGSGVVSTITE 396

sp P64029 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394
EFTU_STAAW (strain
MW2)] AA
align

Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60

MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + + YD IDAP+E+ERG

Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

ITI TSHEIY+T+ RHAYHDCPGHADYVENMTGAAQMDG I LVVSAADGPMPQTREHI

Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180

LLSR VGV+IVVFLNK S Y+FPGDD P++AGSAL+ALE

Sbjct: 121 LLSRNVGVPALVVFLNKCDMVDEELLELVEMEVRLLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIERG 240

++ EK+L+IM VD+YIPTPERD+K F+MPVEDVFSI GRRTV TGR+EERG

Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMMPVEDVFSITGRGTATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
+KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL

Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKL LDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PGSITPH +F+ E+YVLSK+EGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMPGD

Sbjct: 296 PGSITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYRTTDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIE 399
NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+

Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

sp Q6GBT9 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394
EFTU_STAAS (strain AA
MSSA476)] align

Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + + YD IDNAP+EKERG

Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI TSHIEY+T+ RHYAHDCPGHADYVKNMITGAAQMDG I I VVSAADGPMPQTREHI

Sbjct: 61 ITINTSHIEYQTDKRHYAHDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LLSR VGVF +VVELNK S V+FPGDD P++AGSAL+ALE

Sbjct: 121 LLSRNVGVPALVVFNLKVDMVDEELLEVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
++ EK+L+LM VD+YIPTPERD++K F+MPVEDVFSI GRGIV TGR+ERG

Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMMPVEDVFSITGRGTATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
+KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL

Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKL LDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PGSITPH +F+ E+YVLSK+EGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMPGD

Sbjct: 296 PGSITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYRTTDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIE 399
NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+

Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

sp Q6GJC0 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394
EFTU_STAAR (strain AA
MRSA252)] align

Score = 559 bits (1441), Expect = e-158
 Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF+R+ H NIGTIGHV HGKTTL+AII+ VI+ G + + YD IDNAP+EKEKRG
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHIEY+T+ RHYAHDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVF +VVFLNK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVTGRIERG 240
 ++ EK+L+LM VD+YIPTPERD++K F+MFVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GDAQYEKILELMEAVDTYIPTPERDSKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +V+KG VL
 Sbjct: 236 QIKVGEEEVIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLGVAREDVORGQVLAA 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH +P+ E+YVLSK+EGGRHTPFFTNYRPQFY RTTENVG + LPEG EMVMPGD
 Sbjct: 296 PGSITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYRTTDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ TT+
 Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

sp P99152 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394
 EFTU_STAAN (strain AA
N315)] align

Score = 559 bits (1441), Expect = e-158
 Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF+R+ H NIGTIGHV HGKTTL+AII+ VI+ G + + YD IDNAP+EKEKRG
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHIEY+T+ RHYAHDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVF +VVFLNK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVTGRIERG 240
 ++ EK+L+LM VD+YIPTPERD++K F+MFVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GDAQYEKILELMEAVDTYIPTPERDSKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

+KVG+EVEI+G+ T KTTVTGEMFRK L+ EAGDN+G LLRG +E+V+RG VL
 Sbjct: 236 QIKVGEVEIIIGLHDTSKTTVTGEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH +F+ E+YVLSK+EGGRHTPFFTNYRPQFY RPTTDVTG + LPEG EMVMPGD
 Sbjct: 296 PGSITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIIE 399

NV++TVELI+P+A+E GT+F+REGGRTVG+GVV+ II+

Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

sp P64028 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394
 EFTU_STAAM (strain AA
 Mu50 / ATCC 700699)] align

Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRNTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R+ H NIOTIGHV HGKTL+AAI+ VL+ G + + YD IDNAP+EKERG
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHEIY+T+ RHYAHDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVP +VVFLENK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDEELLEVEMEVRDLLSEYDFPGDDVPIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 ++ EK+L+IM VD+YIPTPERD+K F+MPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GDAQYEKILELMEAVENTYIPTPERDSDKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +KVG+EVEI+G+ T KTTVTGEMFRK L+ EAGDN+G LLRG +E+V+RG VL
 Sbjct: 236 QIKVGEVEIIIGLHDTSKTTVTGEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH +F+ E+YVLSK+EGGRHTPFFTNYRPQFY RPTTDVTG + LPEG EMVMPGD
 Sbjct: 296 PGSITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIIE 399

NV++TVELI+P+A+E GT+F+REGGRTVG+GVV+ II+

Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

tr Q5HIC7 Translation elongation factor Tu [tuf] [Staphylococcus] 394
 Q5HIC7_STAAC aureus (strain COL) AA align

Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + + YD IDNAP+EKEKG
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHIEY+T+ RHYAHDCPGHADYVKNMITGAAQMDG I LVVSAADGPMPQTREHI
 Sbjct: 61 ITINTSHIEYQTDKRHYAHDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVF +VVFINK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDEELLELVEVRLLLSEYDFPGDDPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVFSI GRGT V TGR+ERG
 Sbjct: 181 -----GDAQYEKILELMEAVDTYIPTPERDSKPFMMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LRG +E+V+RG VL
 Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKL LDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSTITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSTITPH +F+ E+YVLSK+EGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMPGD
 Sbjct: 296 PGSTITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALEGTKFAIREGGRTVGAGVVSNIIE 399
 NV++TVELI+P+A+E GP+F+IREGGRTVG+GVV+ LI+
 Sbjct: 356 NVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

tr Q5QWA3 Translation elongation factor EF-Tu [tufB_1] [Idiomarina 394 AA
Q5QWA3_IDILO loihiensis] align

Score = 559 bits (1441), Expect = e-158
 Identities = 271/399 (67%), Positives = 325/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 M+KEKF+R+ PRVN+GFTIGHV HGKTTL+AAI+ VL+ KD+ IDNAP+EKEKG
 Sbjct: 1 MSKEKFERSKPHNVGTIGHVDHGKTLTAAITTVLAKVYGGAOKDFAAIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSHIEY+T+ RHYAHDCPGHADYVKNMITGAAQMDG I LVVSAADGPMPQTREHI
 Sbjct: 61 ITISTSHVEYDTPTRHYAHDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP IVVF+NK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRQVGVPFIVVFMNKCDMVDEELLELVEVRELLSEYDFPGDDLPVIQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 + EW +K+++L +D+YIP PERD +K F+MP+EDVFSI+GRGT VVTGR+ERG
 Sbjct: 181 GDE----EWSKKIVELADALDNYIPEPERDIDKPFIMPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +V+ GDE RIVG++ T KTTVTGVEMFRK L+ +G AG+ +G LRGTK++VVERG VL K
 Sbjct: 236 IVRTGDECEIVGMKDTKTTVTGVEMFRKL DEGRAGENIGALLRGTKRDDVERGOVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFNTYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PG+TTPH KFD E+YVLSK+EGGRHTPFT YRPQFY RTTDVTG++ LPEGVEMVMPGD
 Sbjct: 296 PGTITPHTKFEAEVYVLSKDEGGRHTPKGYRPQFYFRTTDVTGAVELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIIE 399
 N+K V+L+E+A++ G +FAIREGGRTVGAGVV S I++
 Sbjct: 356 NLKFVVVDLIAPIAMDEGLRFAIREGGRTVGAGVVSKIMD 394

tr Q6N4Q4 Elongation factor Tu (EC 3.6.1.48) [tuf/ EF-Tu] 396
Q6N4Q4_RHOPA [Rhodopseudomonas AA
palustris] align

Score = 558 bits (1439), Expect = e-158
 Identities = 280/401 (69%), Positives = 323/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PH NIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+EK RG
 Sbjct: 1 MAKAKFERTKPHCNIGTIGHVDHGKTSLTAAITKVLAETGGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYET+ RHYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETQRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLRSRQGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQGVGP +VVFLNK S Y+FPGDD PIV GSAL ALE
 Sbjct: 121 LLARQGVVPALVVFLNKCDMVDDPELLELVEMEVRELLSKYDFPGDDIPIVKGSALE 180

Query: 181 --EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIE 238
 +AK G+ + +L+LM +VD+YIP PER ++ FLMPVEDVFSI+GRGTVTGR+E
 Sbjct: 181 NSDAKLGH----DAILELMRQVDAYIPQPERPIDQPFLMPVEDVFSISGRGTVTGRVE 235

Query: 239 RGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVL 298
 RG++KVGDE+EIVGIR TQKTT TGVEMFRK L++G+AGDN+G LLRGTK+E+VERG VL
 Sbjct: 236 RGILKVGDEIEIVGIRDTQKTTCTGVEMFRKLLDQGQAGDNIALLRGTKREDVERGQL 295

Query: 299 CKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMP 358
 CKPGS+ PH KF+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMP
 Sbjct: 296 CKPGSVKPHTKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDVTGVVHLPEGTEMVMP 355

Query: 359 GDNVKITVELISPVALELGKFAIREGGRTVGAGVVSNIIIE 399
 GDN+ + V LI P+A+E +FAIREGGRTVGAGVV+ IIE
 Sbjct: 356 GDNIAMEVHLIVPIAMEEKLRFAIREGGRTVGAGVVAIIIE 396

tr Q73F98 Translation elongation factor Tu [tuf] [Bacillus cereus] 395
Q73F98_BACC1 (strain AA
ATCC 10987) align

Score = 558 bits (1439), Expect = e-158
 Identities = 275/400 (68%), Positives = 322/400 (79%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF R+ PHVNIGTIGHV HGKT+L+AAI+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTAAITVLAAGGAEARGYDQIDAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYETETRHAYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQVGVPVYIVVFLNKCDMVDEELLELVEVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEVKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 +W K+++LMAEVD+YIPTPER+T+K FLMPVEDVFSI GRGTIV TGR+ERG
 Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +VKVGD VEI+G+ TTGTGVEMFRK L++ +AGDN+G LIRG +E+++RG VI
 Sbjct: 236 IVKVGDVVEIIGLAEEENASTTVGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 K GS+ N KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDVTG I LPEG EMVMPG
 Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDVTGIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVNSIIIE 399
 DNV++T+ELI+P+A+E GTKF+IREGGRTVG GVV+ I+E
 Sbjct: 356 DNVEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

sp Q814C4	Elongation factor Tu (EF-Tu) [tuf] [Bacillus cereus	395
EFTU_BACCR	(strain ATCC	AA
	14579 / DSM 31)	<u>align</u>

Score = 558 bits (1438), Expect = e-158
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KE R+ PHVNIGTIGHV HGKTTL+AAL+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITVLA KAGGAEARGYDQIDAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYETETRHAYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQVGVPVYIVVFLNKCDMVDEELLELVEVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEVKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 +W K+++LMAEVD+YIPTPER+T+K FLMPVEDVFSI GRGTIV TGR+ERG
 Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +VKVGD VEI+G+ TTGTGVEMFRK L++ +AGDN+G LIRG +E+++RG VI
 Sbjct: 236 IVKVGDVVEIIGLAEEENASTTVGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 K GS+ N KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDVTG I LPEG EMVMPG
 Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDVTGIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+T+T+ELI+P+A+E GTKF+IREGGRTVG GV++ I+E
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

sp Q81VT2 Elongation factor Tu (EF-Tu) [tuf] [Bacillus anthracis] 395 AA
 EFTU_BACAN

align

Score = 558 bits (1438), Expect = e-158
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAX KF R+ PHVNIGTIGHV HGKTLAAI+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTLAAITVLAKAGGAEARGYDQIDAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYETETRHAYHDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETETRHAYHDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAI+AL+
 Sbjct: 121 LLSRQVGVPYIVVFLNKCDMVDEELLELVEMEVRDLLSEYGFPGDDIPVIKGALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W K+++LMAEVDFYIPTPER+T+K FLMPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLRLGKKEEVERGMVLC 299
 +VXVGD VEI+G+ TTVTGEMFRK L++ +AGDN+G LLRG +E+++RG VL
 Sbjct: 236 IVKVGDVVEIIGLAEEENASTTVTGEMFRKLLDQAQAGDNIGALLGVAREDIORGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDVTG I LPEG EMVMPG
 Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDVTGIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+T+ELI+P+A+E GTKF+IREGGRTVG GV++ I+E
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

tr Q6HPRO Protein-synthesizing GTPase (Translation elongation 395
Q6HPRO_BACHK factor Tu AA
 (EF-TU) (EC 3.6.5.3) [tufA] [Bacillus thuringiensis align
 (subsp. konkukian)]

Score = 558 bits (1438), Expect = e-158
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAX KF R+ PHVNIGTIGHV HGKTLAAI+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTLAAITVLAKAGGAEARGYDQIDAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

 Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQGVGP+IVVFLNK S Y FPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQGVPYIVVFLNKCDMVDEELLEVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

 Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W K++IMAEVD+YIPTPER+T+K FLMPVEDVFSI GRGTG TGR+ERG
 Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

 Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +VKVGD VEI+G+ TTGEMFRK L++ AGDN+G LLRG +E++RG VL
 Sbjct: 236 IVKVDVVEIIGLAENASTTVGVEMFRKLLDQAQADNIGALLRGVAREDIQRGQVLA 295

 Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDVTG I LPEG EMVMPG
 Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDVTGIIQLPEGTEMVMPG 355

 Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+T+T+T+P+A+G GTKF+IREGGRTVG GVV+ T+E
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

tr Q63H92 Protein-synthesizing GTPase (Translation elongation 395
 Q63H92_BACZZ factor Tu AA
 (EF-Tu) (EC 3.6.5.3) [tufA] [Bacillus cereus (strain align
 ZK)]

Score = 558 bits (1438), Expect = e-158
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

 Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAX KF+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITVLA KAGGAEARGYDQIDAPEERERG 60

 Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI 120
 ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

 Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQGVGP+IVVFLNK S Y FPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQGVPYIVVFLNKCDMVDEELLEVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

 Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W K++IMAEVD+YIPTPER+T+K FLMPVEDVFSI GRGTG TGR+ERG
 Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

 Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +VKVGD VEI+G+ TTGEMFRK L++ AGDN+G LLRG +E++RG VL
 Sbjct: 236 IVKVDVVEIIGLAENASTTVGVEMFRKLLDQAQADNIGALLRGVAREDIQRGQVLA 295

 Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDVTG I LPEG EMVMPG
 Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDVTGIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+---+T+ELI+P+A+E GTKF+IREGGRTVG GVV+ I+E
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

tr Q6MJ00 Translation elongation factor Tu (EC 3.6.1.48) [tuf] 396
Q6MJ00_BDEBA [Bdellovibrio AA
bacteriovorus] align

Score = 557 bits (1436), Expect = e-157
 Identities = 275/400 (68%), Positives = 321/400 (79%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 M+KEKF R PHVNIGTIGHV HGKT+L+AAI+ L+ G A+ YD ID +P+EK RG
 Sbjct: 1 MSKEKFTRNKPHVNIGTIGHVDHGKTTAAITTLAASGKAQAMAYDQIDKSPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTTHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSSADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+PQVGVP +VVF+RK S YEPGDD P+V GSAL+ALE
 Sbjct: 121 LLARQVGVPALVVFMNKVDMVDDKELLELVLEVRELLSKYEFPGDDIPVVKGALKALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
 G+ E G +KLM D+YIP P R +KTFILMPVEDVFSI+GRGTVVTGRIER
 Sbjct: 181 ----GDTSEIGRPAIMKLMEACDTYI PAPVRAVDKTFILMPVEDVFSISGRGTVVTGVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKGDE+EIVGIR TQKTTVTG+EMFRK L++G+AGDN GVLLRGTKKE+VERG VL
 Sbjct: 237 GIVKVGDEIEIVGIRPTQKTTVTGIEMFRKLLDEGQAGDNCGVLLRGTKEDVERGQLV 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMMPG 359
 KPG+-- PHKKF+ E Y+L+KEEGGRHTPFF YRPQFY RPPDVTC TL G EMVMPG
 Sbjct: 297 KPGTVKPHKKFKAEAYILTKEEGGRHTPFFNGYRPQFYFRTTDVTGVCTLKAGTEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+---+T+ELI+P+A+E FAIREGGRTVGAGVV+ I+E
 Sbjct: 357 DKIEVSVELIAPIMAKELRFAIREGGRTVGAGVVTEILE 396

tr Q9F9S8 Eftu [eftu] [EDTA-degrading bacterium] 391 AA
Q9F9S8_9PROT BNC1 align

Score = 557 bits (1435), Expect = e-157
 Identities = 284/399 (71%), Positives = 320/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+EK RG
 Sbjct: 1 MAKGFERTKPHVNIGTIGHVDHGKTSLTAAIT----KYFGEFKAYDQIDAPEEKARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 56 ITISTAHVEYETENRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 115

Query: 121 LLSRQVGVPVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP IVVFLNK S Y+FPGDD PIV GSAL ALE
 Sbjct: 116 LLARQVGVPVPAIVVFLNKVDQVDDPELLELVELEIRELLSKYEFPGDDIPIVKGSALAALE 175

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 ++ +GE + V +LMREVD YIPTFER ++ FLMP+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 176 DSNK-EIGE--DAVRQLMAEVDKYIPTPERPIDQPFLMPIEDVFSISGRGTVVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VVKVG+EVEIVGIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E VERG VL K
 Sbjct: 233 VVKVGEEVEIVGIRPTS KTTVTGVEMFRKLLDQGQAGDNIGALLRGIDREGVERGQVLAK 292

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFNTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGS+TPH KF+ E Y+L+KEEGGRHTPFNTNYRPQFY RTTDVTG +TLPEG EMVMPGD
 Sbjct: 293 PGSVTPHTKFKA EAYILTKEEGGRHTPFNTNYRPQFYRTTDVTGVVTPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + V LI P+A+E +FAIREGGRTVGAG+V++I E
 Sbjct: 353 NVTMDVTLIVPIAMEERLFAIREGGRTVGAGIVASITE 391

tr Q5PIW4 **Elongation factor Tu [tufA] [Salmonella paratyphi-a]** 394 AA
Q5PIW4_SALPA

align

Score = 556 bits (1434), Expect = e-157
 Identities = 272/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 M+KEKF RT PHVN+GTIGHV HGKTL+AAI+ VL+ + +D IDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVTIGHVDHGKTLAAITTVLAKTYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EY+T TRHYAHDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTPTRHYAHDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 EW K++I+DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 -----GDAEWEAKIELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++KVG+EVEIVGIR T QK+T TGEMFRK L++G AG+NVCVLLRG K+EE+ERG VL K
 Sbjct: 236 IIKGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFNTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PG+I PH KFE E+Y+LSK+EGGRHTPFY YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGTIKPHTKFESSEVYILSKDEGGRHTPKGYRPQFYRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 398
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 356 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVAKVL 393

tr Q57H76 Protein chain elongation factor EF-Tu (Duplicate of
Q57H76_SALCH tufA) [tufB]
[*Salmonella cholerae-suis* (*Salmonella enterica*)] 394
AA
align

Score = 556 bits (1434), Expect = e-157
Identities = 272/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
MAKEKF RT PHVN+G+T+G+V NGKTTL+A+V+L+ + +D IDNAP+EK RG
Sbjct: 1 MSKEKFERTKPHVNVTIGHVDHGKTTLAAITVLAKTYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI TSH+EY+T RHAYHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVVFNLKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LL RQVGVP+I+V+FLNK S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
++KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL K
Sbjct: 236 IIKVGEeveIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFNTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PG+I PH KFE E+Y+LSK+EGGRHTPFT YRPQFY RTPDVTG+I LPEGVEMVMPGD
Sbjct: 296 PGTIKPHTKFESEVYILSKDEGGRHTPKGYRPQFYFRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSII 398
N+K+ V LT P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 393

tr Q6N0C2 EF-Tu [orf3309] [*Magnetospirillum*
Q6N0C2_9PROT *gryphiswaldense*] 396 AA
align

Score = 556 bits (1434), Expect = e-157
Identities = 280/399 (70%), Positives = 319/399 (79%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
MAK KE R PH NI GTI GHV NGKT+L+A+V+L+ G A YD ID AP+EK RG
Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTSLTAAITKVLAETGGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI+T+H+EYET RHAYHVDCPGHADYVKNMITGAAQMDG I I VVSAADGPMPQTREHI
Sbjct: 61 ITISTAHVEYETANRHAYHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVVFNLKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LL+RQVGVP +VVF+NK S+Y+FPGDDTPIV GSAL ALE
Sbjct: 121 LLARQVGVPALVVFMNKCDMVDDPELLDLEVLVRELLSSYDFPGDDIPIVRSALCALE 180

Query: 181 EAKAGNVGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240

+ K +G + +L DMAEVG YIP PER +K FLMP+EDVFSI+GRGTVVVTGR+ERG
 Sbjct: 181 D-KQPEIGR--DAILALMAEVVKYIPQPERPKDKPFLMPIEDVFSISGRGTVVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK 300
 VVKVG+EVEIVGI+ T KTF TGVEMFRK L++GEAGDN+G LLRG K++VERG VI
 Sbjct: 238 VVKVGEEVEIVGIKPTVKTTCTGVEMFRKLLDQGEAGDNIGALLRGVKREDVERGQVLAA 297

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH KF E Y+L+KEEGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMPGD
 Sbjct: 298 PGSITPHTKFTAEAYILNKEEGGRHTPFFTNYRPQFYRTTDVTGMVYLPEGTEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV +TV+L+P+A+ G +FAIREGGRTVGAGVV+ IIE
 Sbjct: 358 NVSMTVQLIAPIAMDEGLRFAIREGGRTVGAGVVAIIIE 396

sp P26184 Elongation factor Tu (EF-Tu) [tuf] [Flexistipes 396
 EFTU_FLESI sinusarabici] AA align

Score = 556 bits (1433), Expect = e-157
 Identities = 275/399 (68%), Positives = 325/399 (80%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 M+K+R+ R FHN+GFIGAV HGKTTL+AA++ VLSLK G A+ ++ NID AP+EKERG
 Sbjct: 1 MSKQKYERKKPHVNVTIGHVHDHGKTTLAAMTHVLSLKGYADYIEFGNIDKAPEEKERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAAADGPMPQTREHI 120
 ITIAT+H+EYE++ RHAYHDCPGHADYVKNMITGAAQMDGAILVVSAAADGPMPQTREHI
 Sbjct: 61 ITIATAHVEYESDKRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP IVVF+NK + YEPGDD PI+ GSAL+ALE
 Sbjct: 121 LLARQVGVPVPHIVVFLNKCDMVDEELLELVELEIIRDLLNTYEFPGDDIPIIKGSAQALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSIPTPERDTEKTFLMPVEDVFSIAGRGTVVVTGRIERG 240
 A+ E + +L+ +D YIP PERD +K FLMP+EDVFSI+GRGTVVVTGR+ERG
 Sbjct: 181 NAEDE---EKTLCI WELLQAMDDYIPAPERDIDKPFLMPIEDVFSISGRGTVVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVLCK 300
 V+V DE+EIVG+ T+KT VTGVEMFRK L++GEAGDNVGVLRLRG K++VERG VI K
 Sbjct: 238 KVVRQDEIEIVGLTDTRKTVVTGVEMFRKILDEGEAGDNVGVLRLGIKKDDVERGQVLAK 297

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH+K+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDVTG ITL EGVEMVMPGD
 Sbjct: 298 PGSITPHRKFKCEAYILTKEEGGRHTPFFSGYRPQFYRTTDVTGVITLAEGVEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV +V+LI P+A+G +FAIREGGRTVGAGVV+ I+E
 Sbjct: 358 NISCDVDLIQPIAMEQGLRFAIREGGRTVGAGVTEIVE 396

sp Q83JC4 Elongation factor Tu (EF-Tu) [tufA] [Shigella flexneri] 393 AA
 EFTU_SHIFL align

Score = 555 bits (1431), Expect = e-157
 Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 2 AKEFNRTNPHVNIGTIGHVYHGKTLSSAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61
 +KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI
 Sbjct: 1 SKEKFERTKPHVNVTGIGHVDHGKTLTAITVLAKEYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILLVSAADGPMPQTREHIL 121
 TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILLVV+A DGPMPQTREHIL
 Sbjct: 61 TINTSHVEYDTPTRHAYAHVDCPGHADYVKNMITGAAQMDGAILLVVAATDGPMPQTREHIL 120

Query: 122 LSRQGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
 L RQGVGP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LGRQGVGPYIIIVFLNKCDMVDDEELLELVEMEMEVRELLSQYDFPGDDTPIVRGSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERGV 241
 EW K+L+I+ +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
 Sbjct: 180 ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLCKP 301
 +KVG+EVG+IVGT+ TQK+T TGVEMFRK I++G AG+NVGVLRLG K+EE+ERG VL KP
 Sbjct: 236 IKVGEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAQP 295

Query: 302 GSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTDVTSITLPEGVEMVPGDN 361
 G+I PH KFE E+Y+LSK+EGRNTPFF YRPQFY RTTDVTC+I LPEGVEMVPGDN
 Sbjct: 296 GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVGTIELPEGVEMVPGDN 355

Query: 362 VKITVELISPVAELGTKFAIREGGRTVGAGVVSNII 398
 +K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp <u>P0A6N1</u>	Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia	393
<u>EFTU_ECOLI</u> coli]		AA
		<u>align</u>

Score = 555 bits (1431), Expect = e-157
 Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 2 AKEFNRTNPHVNIGTIGHVYHGKTLSSAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61
 +KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI
 Sbjct: 1 SKEKFERTKPHVNVTGIGHVDHGKTLTAITVLAKEYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILLVSAADGPMPQTREHIL 121
 TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILLVV+A DGPMPQTREHIL
 Sbjct: 61 TINTSHVEYDTPTRHAYAHVDCPGHADYVKNMITGAAQMDGAILLVVAATDGPMPQTREHIL 120

Query: 122 LSRQGVPHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
 L RQGVGP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LGRQGVGPYIIIVFLNKCDMVDDEELLELVEMEMEVRELLSQYDFPGDDTPIVRGSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERGV 241
 EW K+L+I+ +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
 Sbjct: 180 ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLCKP 301

+EVG+EVEIVGT+ TQK+T TGVEMFRK L++G AG+NVGVLRLRG K+EE+ERG VL KP
 Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDN 361
 G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGDN
 Sbjct: 296 GTIKPHTKFSESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 +K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 356 IKMVTTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp P0A6N2 Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia coli O6] 393
 AA align

Score = 555 bits (1431), Expect = e-157
 Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 2 AKEKFNRNPHVNIGTIGHVYHGKTLAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61
 +KEKF RT PHVN+GTIGHV HGKTLAAI+ VL+ + +D IDNAP+EK RGT
 Sbjct: 1 SKEKFERTKPHVNVTIGHVDHGKTLTAITVLAKYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHAYHVDCPGHADYVKNMITGAAQMDGAILLVSAADGPMPQTREHIL 121
 TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILLV+A DGPMPQTREHIL
 Sbjct: 61 TINTSHVEYDTPTRHAYHVDCPGHADYVKNMITGAAQMDGAILLVAAATDGPMPQTREHIL 120

Query: 122 LSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
 L RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LGRQVGVPYIIVFLNKCDMVDDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERGV 241
 EW K+L+I +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
 Sbjct: 180 ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
 +KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLRLRG K+EE+ERG VL KP
 Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDN 361
 G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGDN
 Sbjct: 296 GTIKPHTKFSESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 +K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 356 IKMVTTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp P0A6N3 Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia coli O157:H7] 393
 AA align

Score = 555 bits (1431), Expect = e-157
 Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 2 AKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERGI 61
 +KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGT
 Sbjct: 1 SKEKFERTKPHVNVTGIGHVDHGKTLTAAITVLAKEYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHIL 121
 TT TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHIL
 Sbjct: 61 TINTSHVEYDTPTRHAYHDCPGHADYVKNMITGAAQMDGAILVVAAATDGPMPQTREHIL 120

Query: 122 LSRQVGVPHVFLNXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
 L RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LGRQVGVPYIIVFLNKCDMVDDDEELLELVEVRELLSQYDFPGDDTPIVRGSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERGV 241
 EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
 Sbjct: 180 ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLGKKEEVERGMVLCKP 301
 +KVG+EVEIVGL+ TQK+T TGEMFRK L+G AG+NVGVLRLG K+EE+ERG VL KP
 Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLRLGIKREEIERGQVLA 295

Query: 302 GSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDN 361
 G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+T LPEGVEMVMPGDN
 Sbjct: 296 GTIKPHTKFESEVYIILSKDEGGRHTPFFKGYRPQFYFRTTDVTGIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGKFAIREGGRTVGAGVVSNII 398
 +K+ V LT P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

tr Q5ZYP5	Translation elongation factor Tu (EF-Tu) (EC 3.6.5.3)	396
Q5ZYP5_LEGPH	[tufB]	AA
	[Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152)]	<u>align</u>

Score = 555 bits (1430), Expect = e-157
 Identities = 278/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD TD AP+E+ERG
 Sbjct: 1 MAKEKFERTKPHVNVTGIGHVDHGKTLTAAITTIMAKKYGGTAKAYDQIDAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+E+H+EYE+ +RHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYESASRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 180
 LLSRQVGVP+IVVF+NK S+Y+FPGDD PIV GSAL+ALE
 Sbjct: 121 LLSRQVGVPYIIVVFMNKADMVDDPELLELVEVREDLLSSYDFPGDDIPIVVGALKALE 180

Query: 181 EAKAGNVGEWGEKVL-KLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G + G K + KL+ +DSYIP P R+ +K FL+P+EDVFSI+GRGTVVTGR+E
 Sbjct: 181 ----GEDSDIGVKAIEKLVETMDSYIPEPVRNIDKPFLPIEDVFSISGRGTVVTGRVES 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLGKKEEVERGMVLC 299
 G+VKG+EVEIVGIR TQKTT TGEMFRK L+G AGDNVGVLRLGK++EVERG VL
 Sbjct: 237 GIVKVGEEVEIVGIRDTQKTTCTGVEMFRKLLDEGRAGDNVGVLRLGKDEVERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPG+I PH KFE E+YVLSKEEGGRHTPFF YRPQFY RTTDVTG+ LP GVEMVMPG
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPQFYFRTTDVTGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIIE 399
 DNV++ V L +P+A++ G +FAIREGGRTVGAGVV+ IIIE
 Sbjct: 357 DNVQLVVSLHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q5X873 Translation elongation factor Tu [tufA] [Legionella
Q5X873_LEGPA pneumophila
 (strain Paris)] 396
 AA
align

Score = 555 bits (1430), Expect = e-157
 Identities = 278/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKG LAEMKD YDNIDNA PQE KERG 60
 MAKEKF R PHVN+GTIGHV HGKTTL+AAI+ + + K K YD ID AP+E+ERG
 Sbjct: 1 MAKEKFERKKPHVNVTIGHVDHGKTTLAAITTIMAKKYGGTAKAYDQIDAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYE+ +RHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITISTAHVEYESASRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NNK S+Y+FPGDD PIV GSAL+ALE
 Sbjct: 121 LLSRQVGVPYIIVFMNKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIVVGSALKALE 180

Query: 181 EAKAGNVGEWGEKVL-KLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G + G K + KL+ +DSYIP P R+ +K FL+P+EDVFSI+GRGTVVTGR+E
 Sbjct: 181 ----GEDSDIGVKAIKEKLVETMDSYIPEPVNRIDKPFLPIEDVFSISGRGTVVTGRVES 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLGKKEEVERGMVLC 299
 G+VKVG+EVEIVGIR WQKTT TGVEMFRK L+G AGDNVGVLRLGK++EVERG VI
 Sbjct: 237 GIVKVGEVEIVGIRD TQKTTCTGVEMFRKLLDEGRAGDNVGVLRLGKDEVERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPG+I PH KFE E+YVLSKEEGGRHTPFF YRPQFY RTTDVTG+ LP GVEMVMPG
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPQFYFRTTDVTGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIIE 399
 DNV++ V L +P+A++ G +FAIREGGRTVGAGVV+ IIIE
 Sbjct: 357 DNVQLVVSLHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q57J27 Protein chain elongation factor EF-Tu (Duplicate of
Q57J27_SALCH tufA) [tufB] 409
 [Salmonella cholerae-suis (Salmonella enterica)] AA
align

Score = 555 bits (1430), Expect = e-157
 Identities = 271/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKG LAEMKD YDNIDNA PQE KERG 60
 ++KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG

Sbjct: 16 VSKEKFERTKPHVNVTGIGHVDHGKTLTAAITVLAKTYGGAARAFDQIDNAPEEKARG 75
 Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 TI TSH+YE+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMFQTREHI
 Sbjct: 76 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 135.
 Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 136 LLGRQVGVPYIIVFLNKCDMVDEELLELVEMEVRELLSQYDFPGDDTPIVRGALKALE 195
 Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 196 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERG 250
 Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL K
 Sbjct: 251 IIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLA 310
 Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PG+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 311 PGTIKPHTKFESEVYIILSKDEGGRHTPFFKGYRPQFYRTTDVTGIELPEGVEMVMPGD 370
 Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 N+K+ V LT P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 371 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 408

sp <u>P0A1H5</u>	Elongation factor Tu (EF-Tu) [tufA] [Salmonella	393
EFTU_SALTY	typhimurium]	AA
		<u>align</u>

Score = 555 bits (1429), Expect = e-157
 Identities = 271/397 (68%), Positives = 319/397 (80%), Gaps = 5/397 (1%)

Query: 2 AKEFNRTNPHVNIGTIGHVYHGKTLAAISAVSLSLKGLAEMKDYNIDNAPQEKERGI 61
 +KEKF RT PHVN+GTIGHV HGKTL+AAI+ VL+ + +D IDNAP+EK RGI
 Sbjct: 1 SKEKFERTKPHVNVTGIGHVDHGKTLTAAITVLAKTYGGAARAFDQIDNAPEEKARGI 60
 Query: 62 TIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHIL 121
 TI TSH+YE+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMFQTREHIL
 Sbjct: 61 TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHIL 120
 Query: 122 LSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
 LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LGRQVGVPYIIVFLNKCDMVDEELLELVEMEVRELLSQYDFPGDDTPIVRGALKALE- 179
 Query: 182 AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERGV 241
 EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
 Sbjct: 180 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERGI 235
 Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
 ++KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP
 Sbjct: 236 IKGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLA 295
 Query: 302 GSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDN 361
 G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGDN

Sbjct: 296 GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398

+X+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++

Sbjct: 356 IKMVVTЛИHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp P0A1H6 Elongation factor Tu (EF-Tu) [tufA] [Salmonella typhi] 393 AA
EFTU_SALTI

align

Score = 555 bits (1429), Expect = e-157

Identities = 271/397 (68%), Positives = 319/397 (80%), Gaps = 5/397 (1%)

Query: 2 AKEFNRTNPHVNIGTIGHVYHGKTLAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61
+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D TDNAP+EK RGI

Sbjct: 1 SKEKFERTKPHVNVTIGHVHDHGKTLAAITVLAKEYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAI LVVSAADGPMPOTREHIL 121
T TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAI LVV+A DGPMPQTREHIL

Sbjct: 61 TINTSHVEYDTPTRHAYAHVDCPGHADYVKNMITGAAQMDGAI LVVAATDGPMPQTREHIL 120

Query: 122 LSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
L RQVGVP+T+VFLNK S Y+FPGDDTPIV GSAL+ALE

Sbjct: 121 LGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSAKALE- 179

Query: 182 AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERGV 241
EW K++L +DSYIP PER +K FL+F+EDVFSI+GRGTVVTGR+ERG+

Sbjct: 180 ----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGLLRGTKKEEVERGMVLCKP 301
+XVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLRG K+E+ERG VL XP

Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGLLRGKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDN 361
G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGDN

Sbjct: 296 GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398

+X+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++

Sbjct: 356 IKMVVTЛИHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp O31298 Elongation factor Tu (EF-Tu) [tuf] [Buchnera aphidicola] 394
EFTU_BUCAP (subsp.
Schizaphis graminum)] AA
align

Score = 555 bits (1429), Expect = e-157

Identities = 272/398 (68%), Positives = 318/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEFNRTNPHVNIGTIGHVYHGKTLAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
+KEKF R PH+N+GTIGHV HGKTTL+AAI+ VLS K + +D TDNAP+EK RGI

Sbjct: 1 MSKEKFQRVKPHINVGTIGHVHDHGKTLAAITVLSKKYGGSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYAHVDCPGHADYVKNMITGAAQMDGAI LVVSAADGPMPQTREHI 120

ITI TSH+EV+TE RHYAHVDCPGHADY+KNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTELRYAHVDCPGHADYIKNMITGAAQMDGAILVVAADGPMPQTREHI 120

 Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL: RQGVGP+I+VFLNK + Y+FPGDDTP+ GSAL+ALE

 Sbjct: 121 LLGRQGVVPYIIVFLNKCDMVDEELLEVEMEVRDLLTQYDFPGDDTPIRGSALKALE 180

 Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 +W K+L +D+YIP P+R ++ FL+P+EDVFSI+GRGTVTGR+ERG

 Sbjct: 181 -----GDADWESKILDLSKFLDTYIPEPKRAIDQPFLPIEDVFSISGRGTVTGRVERG 235

 Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VKVG+EVEIVGI+ T KTT TGVEMFRK L+G AG+NVGVLRLGTK+E+ERG VL K

 Sbjct: 236 IVKVGEEVEIVGIKKTTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVLAK 295

 Query: 301 PGSIYPHKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PH PE E+YVLSKEEGGRHTPFFT YRPQFY RTTDVTGSI LPEGVEMVMPGD

 Sbjct: 296 PGSIYPHTTSEVYVLSKEEGGRHTPFKGYRPQFYRTTDVTGSIELPEGVEMVMPGD 355

 Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 N+K+TV LI P+A+ G +FAIREGGRTVGAGVVS ++

 Sbjct: 356 NIKMTVTLIHPIAMADGLRFAIREGGRTVGAGVVSKVL 393

tr Q6FZC0 Elongation factor tu (EF-tu) [tuf1] [Bartonella quintana 391 AA
Q6FZC0 _BAROU (Rochalimaea quintana)]

align

Score = 555 bits (1429), Expect = e-157
 Identities = 277/399 (69%), Positives = 322/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KP RT PHVNIGTIGHV HGKT+L+AAL+ X B K ND ID AP+E+ RG
 Sbjct: 1 MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAPEERARG 55

 Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAADGPMPQTREHI 120
 ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVAADGPMPQTREHI
 Sbjct: 56 ITISTAHVEYETEKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAADGPMPQTREHI 115

 Query: 121 LLSRQGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL: RQGVGP IVVFLNK S Y+FPGDD PIV GSAL ALE

 Sbjct: 116 LLARQGVPAIVVFLNKDVQVDDAELLELVELEIRELLSKYDFPGDDIPIVKGSAALAE 175

 Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 * K ++GE + V LM+EV+YIPTPER ++ FL+P+EDVFSI+GRGTVTGR+ERG
 Sbjct: 176 D-KDKSIGE--DAVRLLMSEVDNYIPTPERPVDQFLLPIEDVFSISGRGTVTGRVERG 232

 Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+KVG+E+ET+GLR T KTTVTGVEMFRK L+G+AGDN+G LIRG +E +ERG VL K
 Sbjct: 233 VIKVGEEIEIIGIRPTSCKTGTGVEMFRKLLDQGQAGDNIGALLRGVDREGIERGQVLAK 292

 Query: 301 PGSIYPHKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSIYPHKFEEEIYVLSKEEGGRHTPFFTNYRPQFY RTTDVTGSI LPEGVEMVMPGD

 Sbjct: 293 PGSVTPHTRKAEAYILTKDEGGRHTPFFTNYRPQFYRTTDVTGIVTLPEGIEMVMPGD 352

 Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 399

NV + V LI P+A+S +FAIREGGRTVGAG+VS IIE
 Sbjct: 353 NVAMDVLIVPIAMEEKLRFAIREGGRTVGAGIVSKIIE 391

tr Q5WZL4 Elongation factor Tu [tufA] [Legionella pneumophila] 396
Q5WZL4_LEGPL (strain Lens) AA
align

Score = 555 bits (1429), Expect = e-157
 Identities = 277/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD ID AP+E+ERG

Sbjct: 1 MAKEKFERKKPHVNIGTIGHVHDHGKTTLAAITTIMAKKYGGTAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYE+ +RHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITISTAHVEYESASRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NK S+Y+FPGDD PI+ GSAL+ALE

Sbjct: 121 LLSRQVGVPYIVVFMNKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIIIVGSALKALE 180

Query: 181 EAKAGNVGEWGEKVL-KLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G + G K + KL+ +DSYIP P R+ +K FL+P+SDVFSI+GRGTVVTGR+E

Sbjct: 181 ----GEDSDIGVKAIKEKLVETMDSYIPEPVRNIDKPFLIEDVFSISGRGTVVTGRVES 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKVG+EVEIVGIR TQKTT TGVEMFPK L++G AGEINVGVLLRGTK++EVERG VL

Sbjct: 237 GIVKVGEEVEIVGIRDTQKTTCTGVEMFRKLLDEGRAGDNVGVLLRGTKRDEVERGQVLA 296

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KFG+I PH KFE E+YVLSKEEGGRHTPFF YRPQFY RTTDVTG+ LF GVEMVMPG

Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPQFYFRTTDVTGTCCLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSIIE 399
 DNV++ V L +P+A++ G +FAIREGGRTVGAGVV+ IIE

Sbjct: 357 DNVQLVVSILHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

sp Q925Y6 Elongation factor Tu (EF-Tu) [tufA] [Rhizobium meliloti] 391 AA
EFTU_RHIME (Sinorhizobium meliloti))
align

Score = 554 bits (1428), Expect = e-156
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF R PHVNIGTIGHV HGKTTL+AAI+ K E K YD ID AP+EK RG

Sbjct: 1 MAKSKFERNKPHVNIGTIGHVHDHGKTSLTAAIT----KYFGEFKAYDQIDAPEEKARG 55

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYE+ RHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 56 ITISTAHVEYETPNRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 115

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP IVVFLNK S+YFFGDD PIV GSAL ALE
 Sbjct: 116 LLARQVGVPVHIVVFLNKVDQVDDAELLELVELEVRELLSSYEFPGDDIPIVKGSALAALE 175

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 ++ +GE + + +IMA VD+YIPTPER + + FIMP+EVDVFSI+GRGTVTGR+ERG
 Sbjct: 176 DSDK-KIGE--DAIRELMAAVDAYIPTPERPIDQPFLMPIEDVFSISGRGTVTGRVERG 232.

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VKVG+E+ELVGIR T KTT GVEMFRK L++G+AGDN+G LARG + VERG +LCK
 Sbjct: 233 IVKGEEIEIVGIRPTKTTCTGVEMFRKLLDQGQAGDNIGALLRGVDRNGVERGQILCK 292

Query: 301 PGSIYPKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGS+ PH+KF+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDVTG +TLPEG EMVMPGD
 Sbjct: 293 PGSVKPHRKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDVTGIVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + VELI P+A+E +FAIREGGRTVGAG+V+ +I+E
 Sbjct: 353 NTVVDVELIVPIAMEEKLRFAIREGGRTVGAGIVASIVE 391

tr Q6FZL2 **Elongation factor tu (EF-tu) [tuf2] [Bartonella quintana 391 AA**
Q6FZL2_BARQU **(Rochalimaea quintana)**

align

Score = 554 bits (1428), Expect = e-156
 Identities = 277/399 (69%), Positives = 322/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTLAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PHVNIGTIGHV HGKT+L+AAI+ K S K YD ID AP+E+ RG
 Sbjct: 1 MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEERARG 55

Query: 61 ITIATSHIEYETETRHAYVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 56 ITISTAHVEYETEKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 115

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP IVVFLNK S+YFFGDD PIV GSAL ALE
 Sbjct: 116 LLARQVGVPVHIVVFLNKVDQVDDAELLELVELEVRELLSSYEFPGDDIPIVKGSALAALE 175

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 + K ++GE + V IM+EVD+YIPTPER + + FL+P+EVDVFSI+GRGTVTGR+ERG
 Sbjct: 176 D-KDKSIGE--DAVRLLMSEVDNYIPTPERPIDQPFLMPIEDVFSISGRGTVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VKVG+E+ELVGIR T KTT GVEMFRK L++G+AGDN+G LARG +E +ERG VL K
 Sbjct: 233 VIKGEEIEIIGIRPTKTTVTGVEMFRKLLDQGQAGDNIGALLRGVDREGIERGQVLAK 292

Query: 301 PGSIYPKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGS+PH+ +F+ E Y+L+K+EGGRHTPFFTNYRPQFY RTTDVTG +TLPEG+EMVMPGD
 Sbjct: 293 PGSVTPHTRFKAEAYILTKEDEGGRHTPFFTNYRPQFYFRTTDVTGIVTLPEGIEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + V LI P+A+E +FAIREGGRTVGAG+V+ IIE
 Sbjct: 353 NVAMDVSLLIVPIAMEEKLRFAIREGGRTVGAGIVSKIIE 391

tr Q7MYE8 Elongation factor Tu (EF-Tu) [tufA] [Photorhabdus 394
Q7MYE8_PHOLL luminescens AA
 (subsp. laumontii)] align

Score = 554 bits (1428), Expect = e-156
 Identities = 269/398 (67%), Positives = 321/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 M+AKSKF RT PHVN+G+TIGHV HGKTTL+AII+ VL+ + +D EDNAAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVTGIGHVDHGKTTLAAITVLAKTYGGNARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHDYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+TSH+EY+T +RHYAHDYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITISTSHVEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFLNK S Y+FPGDDTP++ GSAL+ALE
 Sbjct: 121 LLGRQVGVPVHIVVFLNKCDMVDEELLEVEMEVRELLSQYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 -----GDAEWEAKIIELAEALDSYIPEPERAIDQPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VKVG+EVEIVGI+ T KTT TGVEMFRK L++G AG+NVGVLPGTK++E+ERG VL K
 Sbjct: 236 IVKVGEEVEIVGIKDTTCTGEMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVLAK 295

Query: 301 PGSIYPKKFEEEIYVLSKEEGGRHTPFNTYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PH FS E+Y+LSK+EGGRHTPFY YRPQFY RPTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSIKPHTTSESEVYILSKDEGGRHTPKGYRPQFYFRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 N+++ V LI+F+A++ G +FAIREGGRTVGAGV+ +I
 Sbjct: 356 NIQMVKTLIAPIAMDQGLRFAIREGGRTVGAGVVAKVI 393

sp P18668 Elongation factor Tu (EF-Tu) [tuf] [Synechococcus sp. 409
EFTU_SYN P6 (strain PCC AA
 6301) (Anacystis nidulans)] align

Score = 554 bits (1427), Expect = e-156
 Identities = 278/409 (67%), Positives = 328/409 (79%), Gaps = 10/409 (2%)

Query: 1 MAKEKFNRTNPVNIGTIGHVYHGKTTLSAAISAVSLKGLAEMKDYNIDNAPQEKEKRG 60
 MA+ KF RT PH NI GTIGHV HGKTTL+AII+ VL+ G+A+ + Y +ID AP+EK RG
 Sbjct: 1 MARAKFERTKPHANIGTIGHVDHGKTTLAAITVLAKAGMAKARAYADIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHDYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+H+EY+T RHYAHDYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 61 ITINTAHVEYETGNRHYAHDYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S+Y+FPGDD TPIVAGSAL+ALE
 Sbjct: 121 LLAKQVGVPNIVVFLNKEDMVDDAELLELVELEVRELLSSYDFPGDDIPIVAGSALQALE 180

Query: 181 EAKAGNVGE----WGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTG 235
 + G G+ W +K+LKLML EVD+YIPTPER+ ++ FLM VEDVF+I GRGTV TG
 Sbjct: 181 AIQGGASGQKGDNPWVKILKLMEEVDAYIPTPEREVDRPFLMAVEDVFTITGRGTVTG 240

Query: 236 RIERGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERG 295
 RIERG VKVG+ +EIVG+R T+ TTVTGVEMF+K L++G AGGNVG+LRLG +K +ERG
 Sbjct: 241 RIERGSVKVGETIEIVGLRDTSTTGTGVEMFQKTLDEGLAGDNVGLLRGIQKTDIERG 300

Query: 296 MVLCKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSI---TLPEG 352
 MVL KPGSITPH KFE E+YVL KEERGGRRHTEPF YRFQFYVRTTDVTG+I T +G
 Sbjct: 301 MVLAKPGSITPHTKFESEEVYVLKKEEGGRHTPFFPGYRPQFYVRTTDVTGAISDFTADDG 360

Query: 353 --VEMVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 EMV+PGD +K+TVELI+P+A+E G +FAIREGGRT+GAGVVS I++
 Sbjct: 361 SAAEMVIPGDRIKMTVELINPIAIEQGMRFAIREGGRTIGAGVVSILQ 409

sp O31297 Elongation factor Tu (EF-Tu) [tuf] [Buchnera aphidicola] 394
 EFTU_BUCAI (subsp.
 Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium)] AA align

Score = 554 bits (1427), Expect = e-156
 Identities = 270/398 (67%), Positives = 319/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 M+KEKF R PH+N+GTIGRV HCKPTL+AII+ VLS K + +D TDNAP+EK RG
 Sbjct: 1 MSKEKFQLKPHINVGTIGHVDHGKTLTAAITVLSKKFGGSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHAYHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EY+TE RHAYHVDCPGHADY+KNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTEFRHYAHVDCPGHADYIKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL: RQVGVP+I+VFLNK + Y+FPGDDTP+ GSAL+ALE
 Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDEELLEVEMEVRDLLTQYDFPGDDTPIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 EW K++ L +DSYIP P+R ++ FL+F+EDVFSI+GRGTVTG+E+G
 Sbjct: 181 GDP----EWESKIIDLSKFLDSYIPEPKRAVDQFLLPIEDVFSISGRGTVTGRVEKG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMLCK 300
 ++KVG+EVEIVGI+ T KTT TGVEMFRK L++G AG+NVGVLLRGK++E+ERG VL K
 Sbjct: 236 IIKVGEVEIVGIKKTTKTTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSI-LPEGVEMVMPGD 360
 PGSI PH FE E+YVL SKERGGRRHTEPF YRFQFY RTTDVTGSI LPEG+EMVMPGD
 Sbjct: 296 PGSIHPHTTSESEVYVLSKEEGGRHTPFFKGYRPQFYVRTTDVTGSI-LPEGIEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 398
 N+K+TV LI+P+A+ G +FAIREGGRTVGAGVVS ++
 Sbjct: 356 NIKMTVTLINPIAMADGLRFAIREGGRTVGAGVVSILQ 393

sp P33165 Elongation factor Tu (EF-Tu) [tuf] [Bacteroides fragilis] 394 AA

EFTU_BACFR

align

Score = 553 bits (1426), Expect = e-156
 Identities = 271/399 (67%), Positives = 317/399 (78%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVLSLKGLAEMKDYNIDNAPQEKEKRG 60
 MAKEKF RT PHVNIGTIGHV HGKTTL+AAI+ VI+ KGL+E++ +D+IDNAP+EKEKG

Sbjct: 1 MARAKFERTKPHANIGTIGHVDHGKTLAAITVLAKAGMAKARAYADIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSH+EYET RHYAHVDCPGHADYVKNM+TGAAQMDGAI+VV+A DGFMPQTREHI

Sbjct: 61 ITINTAHVEYETGNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQV VP +VVF+NK S Y+F GD+PTI+ GSAL AL

Sbjct: 121 LLARQVNPKLVFFMNKCDMVEDAEMLELVEMEMRELLSFYDFDGDNTPIIQGSALGALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 V +W +KV++IM VD++IP P RD +K FLMPVVDVEST GRGTV TGRIE G

Sbjct: 181 -----GVEKWEDKVMELMEAVDTWIPLPPRVDKFLMPVEDVFSITGRGTVATGRIETG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+ VGDE+E+G+ +K+ VTGVEMFRK L++GEAGDNVG+LLRG K E++RCMVLC

Sbjct: 236 VIHVGDEIEILGLGEDKKSVVTGVEMFRKLLDQGEAGDNVGLLLGVVDKNEIKRCMVLC 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVPGD 360
 PG I PH KF+ E+Y+L KEEGGRATPF YRPQFY+RT D TG ITLPEG EMVMPGD

Sbjct: 296 PGQIKPHSKFKAEVYILKKEEGGRHTPFHNKYRPQFYLRTMDCTGEITLPEGTEMVPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

NV ITVELT FVAL +G +FAIREGGRTVGAG ++ II+

Sbjct: 356 NVTITVELIYPVALNIGLRFaireggRTVGAGQITEIID 394

sp P33171 Elongation factor Tu (EF-Tu) [tuf] [Synechococcus sp. 409
 EFTU_SYN P7 (strain PCC AA
7942) (Anacystis nidulans R2)] align

Score = 553 bits (1424), Expect = e-156
 Identities = 277/409 (67%), Positives = 328/409 (79%), Gaps = 10/409 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVLSLKGLAEMKDYNIDNAPQEKEKRG 60
 MA+ KF RT PH NIGTIGHV HGKTTL+AAI+ VI+ C+A+ + Y +ID AP+EK RG

Sbjct: 1 MARAKFERTKPHANIGTIGHVDHGKTLAAITVLAKAGMAKARAYADIDAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI T+H+EYET RHYAHVDCPGHADYVKNM+TGAAQMDGAI+VV+A DGFMPQTREHI

Sbjct: 61 ITINTAHVEYETGNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQV VP +VVF+NK S Y+F PGDD PIVAGSAL+ALE

Sbjct: 121 LLAKQVGVPNIVVFLNKEDMVDDAELLELVELEVRELLSSYDFPGDDIPIVAGSALQALE 180

Query: 181 EAKAGNVGE----WGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTG 235
 + G G+ W +K+LKLMAEVDSYIPTPER+ ++ FLM VEDVF+I GRGTV TG

Sbjct: 181 AIQGGASGQKGDNPWVDKILKLMEEVDAYIPTPEREVDRPFLMAVEDVFTITGRGTVATG 240

Query: 236 RIERGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERG 295
RIERG VKVG+ +EIVG+R T+ TTVTGVEMF+K L++G AGDNVG+ILRG +K ++ERG
Sbjct: 241 RIERGSVKVGETIEIVGLRDTRSTTVTGVEMFQKTLDEGLAGDNVGLLRGIQKTDIERG 300

Query: 296 MVLCKPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSI---TLPEG 352
MVL KPGSITPH KFE E+YVL N+EGGRHTPFFF YRPQFYVRTTDVTG+I T +G
Sbjct: 301 MVLAKPGSITPHTKFSEVEYVLKKDEGGRRHTPFFPGYRPQFYVRTTDVTGAISDFTADDG 360

Query: 353 --VEMVMPGDNVKITVELISPVALEGTKFAIREGGRTVGAGVVSNII 399
EMV+PGD +K+TVELL+P+A+E G +FAIREGGRT+GAGVV S I++
Sbjct: 361 SAAEMVIPGDRIKMTVELINPIAIEQGMRFIAIREGGRTIGAGVVSKILQ 409

sp Q8ZAN8 Elongation factor Tu-B (EF-Tu-B) [tufB] [Yersinia pestis] 394 AA
EFTU2_YERPE align

Score = 553 bits (1424), Expect = e-156
Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPVNIGHTIGHVYHGKTLSSAIAISAVLSSLKGLAEMKDYNIDNAPQEKERG 60
M+KEKE RT PVVN+GTIGHV HGKTL+AII+ VL+ + +D IDNAP+EK RG
Sbjct: 1 MSKEKFERTKPHVNVTIGHVDHGKTLTAITVLAKTYYGGSARAFDOIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMQPOTREHI 120
TPI TSH+EY+P RHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMQPOTREHI
Sbjct: 61 ITINTSHVEYDTPARHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMQPOTREHT 120

Query: 121 LLSRQVGVPHIIVFLNKXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+-VFLNK S Y+FPGDDTP++ GSAL+ALE
Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSOYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
EW K+++L +DSYTP PER ++ FL+P+EUVFSI+GRGTIVVTGR+ERG
Sbjct: 181 -----GDAEWEAKTIEIAEALDSYIPOPERAIDRPELLPIEDVFSIISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNGVLLRGTKKEEVERGMVLCK 300
 +VVKVG+EVEIVGI T KTT TGDEMFRK L++G AG+NVGVLRLGTK+++V+RG VL K
 Sbjct: 236 IVKVGFEEVEIVGILDTIKTTCTGVEMFRKLLEDEGRAGENVGVLRLGTKRDDVORGVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
PGSI PH KFE E+Y+LSK+EGGRHTPFF YRFQFY RTTIDVTG+I LPEGVEMVMPGD
Sbjct: 296 PGSIKPHTFEESEVYLISKDEGGRHTPEEKGYPRQFYRTTIDVTG+I LPEGVEMVMPGD 355

```

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIE 399
          NV + V LI+P+A++ G +FAIREGGRTVGAGVV+ +IE
Sbjct: 356 NVNMVYHLLRILAMDDGICREIREGGRTVGAGVVSNIE 394

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tr Q66FQ9 Elongation factor Tu [tufA] [Yersinia 394
Q66FQ9_YERPS pseudotuberculosis] AA align

Score = 553 bits (1424), Expect = e-156

Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 M+KEKF RT PHVN+G+TGHV HGKTTL+AAT+ VL+ + +D TDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVTIGHVDHGKTLAAITVLAKTYGGSSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI TSW+EY+T RHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTPARHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+L+VFLNK S Y+FPGDDTP++ GSAL+ALE
 Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDEELLELVEVRELLSQYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVTGK+ERG
 Sbjct: 181 -----GDAEWEAKIEELAEALDSYIPQPERAIDRPFLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VKVG+EVEIVGT T KTT TGVEMFRK L+G AG+NVGVLLRGTK+++V+RG VL K
 Sbjct: 236 IVKVGEEVEIVGIIDTIKTTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDDVORGQVLAK 295

Query: 301 PGSIKPHKKFEEEIYVLSKEEGGRHTPFNYRPQFYVRTDTGSITLPEGVEMVMPGD 360
 PGSI PH KFE E+Y+LSK+EGGRHTPFY YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSIKPHKFSESEVYILSKDEGGRHTPKGYRPQFYRTTDVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + V LI+P+A++ G +FAIREGGRTVGAGVV+ +IE
 Sbjct: 356 NVNMVVNLIAPIAMDDGLRFAIREGGRTVGAGVVAKIE 394

tr Q8KHX9 Elongation factor TU (EF-Tu) [tufB] [Bartonella henselae 391 AA
Q8KHX9_BARHE (Rochalimaea henselae)]

align

Score = 552 bits (1423), Expect = e-156
 Identities = 278/399 (69%), Positives = 320/399 (79%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PHVNIGTIGNV HGKT+L+AAT+ K E K YD ID AP+E+ RG
 Sbjct: 1 MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEERARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+EY+T+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI
 Sbjct: 56 ITISTAHVEYETEKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 115

Query: 121 LLSRQVGVPHVFLNKXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP IVVFLNK S Y+FPGDD PIV GSAL ALE
 Sbjct: 116 LLARQVGVPAIIVFLNKVDQVDDAELLELEVRELLSKYDFPGDDIPIVKGSAALALE 175

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 + K +GE + V LM+EVD+YIPTPER ++ FLMP+EDVFSI+GRGTVTGK+ERG
 Sbjct: 176 D-KDKSIGE--DAVRLLMSEVDNYIPTPERPVDQFLMPIEDVFSISGRGTVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+VKVG+EVEI+GIR T KTTTGEMFRK L+G+AGDN+G LLRG +E +ERG VL K

Sbjct: 233 VIKVGEEVEIIGIRPTSKTTVTGVEMFRKLLDQGQAGDNIGALLRGIDREGIERGQVLAK 292

Query: 301 PGSIYPKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
P S+TPH +F+ E Y+L+K+EEGGRTPEFTNYRPQFY RTTDVTG +TLPEG EMVMPGD

Sbjct: 293 PASVTPHTRFKAEAYILTKDEGGRHTPFTNYRPQFYFRTTDVTGIVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

NV + V LI P+A+E +FAIREGGRTVGAG+VS IIIE

Sbjct: 353 NVAMDVSILVPIAMEEKLRFAIREGGRTVGAGIVSKIIE 391

tr Q89J82 Elongation factor TU [tuf] [*Bradyrhizobium japonicum*] 396 AA
Q89J82_BRAJA

align

Score = 552 bits (1423), Expect = e-156

Identities = 276/401 (68%), Positives = 321/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYDNIDNAPQEKEARG 60
MAK KF R PH NIGTIGHV HGKT+L+AAI+ +L+ G A YD ID AP+EK RG

Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTSLTAAITKILAETGGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI

Sbjct: 61 ITISTAHVEYETKNRHAYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120

Query: 121 LLSRQVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALALE 180
LL+RQVGP +VVFLNK S YEPGD PI+ GSAL ALE

Sbjct: 121 LLARQVGVPALVVFLNKCDMVDDPELLELVELEVRELLSKYEFPGDKIPIIKGSAALALE 180

Query: 181 EA--KAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVTGRIE 238
++ K G+ + +L+LM VD YIP PER ++ FLMPVEDVFSI+GRGTVTGR+E

Sbjct: 181 DSDKKLGH----DAILELMRNVDEYIPIPQPERPIDQPFMLPVEDVFSISGRGTVTGRVE 235

Query: 239 RGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLRLRGTKKEEVERGMVL 298
RG+VAVG+E+EIVG+RATQKTTVTGVEMFRK L++G+AGDN+G LIRGTY+E+VERG VI

Sbjct: 236 RGIVKVGEIEIVGLRATQKTTVTGVEMFRKLLDQGQAGDNIGALLRGTKREDVERGQL 295

Query: 299 CKPGSITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMP 358
CKPGS+ PH KF+ E Y+L+KEEGGRHTPFTNYRPQFY RTTDVTG + LPEG EMVMP

Sbjct: 296 AKPGSVKPHTKFKAEEAYILTKEEGGRHTPFTNYRPQFYFRTTDVTGVVHLPEGTEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

GDN+ + V LI P+A+E +FAIREGGRTVGAGV+V+IE

Sbjct: 356 GDNIAMEVHLIVPIAMEEKLRFAIREGGRTVGAGVVASIIE 396

tr Q727D5 Translation elongation factor Tu [tuf] [*Desulfovibrio vulgaris* (strain Hildenborough / ATCC 29579 / NCIMB 8303)] 397
Q727D5_DESVH AA
align

Score = 552 bits (1423), Expect = e-156

Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 2/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYDNIDNAPQEKEARG 60

M KEKF R PHVNIGTIGH+ HGKTTL+AAI+ L G + YD ID AP+EKRG
 Sbjct: 1 MGKEKFERKKPHVNIGTIGHIDHGKTLTAAITKTAGLLGQGKFIAYDEIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITIAT+S+EYET TRHYAHDVDCPGHADY+KNNMITGAAQMDGAI+VV+A DGPMPQTREHI

Sbjct: 61 ITIATAHVEYETATRHYAHDVDCPGHADYIKNMITGAAQMDGAIIVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+IVVFLNK +Y FFGDD P+V GSAL+ALE

Sbjct: 121 LLARQVGVPVHIVVFLNKCDMVDEELLELVELEVRELLTSYGFPGDDPVVVRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 + + + + +L+A DSYIP P+RD +K FLMP+EDVFSI+GRGTVTGR+ERG

Sbjct: 181 SDDPNS--DACKPIRELLAACDSYIPEPQRDIDKPFLMPIEDVFSISGRGTVTGRVERG 238

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+KVG+EVEIVG+ T K+T TGVEMFRK L++G+AGDN+G LRG K++VERG VI.

Sbjct: 239 VIKVGEVEIVGIKDTTKSTCTGVEMFRKLLDQGQAGDNIGALLRGVKRDDVERGQVLAA 298

Query: 301 PGISITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 P STTPH+K+ + E+YVLSKEEGGRHTPFT+ YRPQFY RTTD+TG ITL EGVEMVMPGD

Sbjct: 299 PKSITPHRKFKAEVYVLSKEEGGRHTPFFSGYRPQFYRTTDITGVITLEEGVEMVMPGD 358

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSIIE 399
 N VELT+P+A+ELG +FAIREGGRTVGAGVVS I+E

Sbjct: 359 NATFNVELIAPIAMELGLRFAIREGGRTVGAGVVSEIVE 397

tr <u>Q7N9B1</u>	Translation elongation factor EF-Tu.B [tufB]	394
Q7N9B1_PHOLL	[Photorhabdus	AA
	luminescens (subsp. laumontii)]	<u>align</u>

Score = 552 bits (1422), Expect = e-156
 Identities = 268/398 (67%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLAAISAVSLKGLAEMKDYNIDNAPQEKG 60
 M+KEKF R PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG

Sbjct: 1 MSKEKFERKKPHVNIGTIGHVHDGKTLTAAITVLAKFVGGNARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+TSH+EY+T +RHYAHDVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI

Sbjct: 61 ITISTSHVEYDTPSRHYAHDVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFLNK S Y+FPGDDTP++ GSAL+ALE

Sbjct: 121 LLGRQVGVPVHIVVFLNKCDMVDEELLELVELEVRELLSQYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVTGRIERG 240
 EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVTGR+ERG

Sbjct: 181 -----GDAEWEAKIIELAEALDSYIPEPERAIDQPFLPIEDVFSISGRGTVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+KVG+EVEIVG+ T K+T TGVEMFRK L++G AG+NVCVLLRGTK++E+ERG VI. K

Sbjct: 236 IVKVGEVEIVGIKDTTKSTCTGVEMFRKLLDEGRAGENVGVLRLGTRDEIERGQVLAK 295

Query: 301 PGISITPHKKFEEEIYVLSKEEGGRHTPFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

PGST PH FB E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSIKPHTTTESEVYILSKDEGGRHTPFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 398
 N+++ V LI+P+A++ G +FAIREGGRTVGAGVV+ +I
 Sbjct: 356 NIQMKVTLIAPIAMDQGLRFAIREGGRTVGAGVVAKVI 393

sp Q8UE16 Elongation factor Tu (EF-Tu) [tufA] [Agrobacterium 391
 EFTU_AGRT5 tumefaciens AA
 (strain C58 / ATCC 33970)] align

Score = 551 bits (1421), Expect = e-156
 Identities = 274/399 (68%), Positives = 320/399 (79%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTLSSAAISAVSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF R PRVNIGTIGHV HGKT+L+AAT+ K E K YD TD AP+EK RG
 Sbjct: 1 MAKSKFERNKPHVNIGTIGHVDHGKTSLTAAIT----KYFGEFKAYDQIDAPEEKARG 55

Query: 61 ITIATSHIEYETETRHAYHDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHI 120
 ITI+T+R+EYET RHYAHDCPGHADYVKNMITGAAQMDGAILV SAADGPMPQTREHI
 Sbjct: 56 ITISTAHVEYETPARHYAHDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQTREHI 115

Query: 121 LLRSRQGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQGVGP IVVFLNK S+Y+FPGDD PT+ GSAL ALE
 Sbjct: 116 LLARQGVGPAIVVFLNKVDQVDDAELLELVELEVRELLSSYDFPGDDIPIIKGSALAALE 175

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 ++ +GE + + +LMA VD+YIPTPER ++ FLMP+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 176 DSDK-KIGE--DAIRELMAAVDAYIPTPERPIDQFLMPIEDVFSISGRGTVVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VKVG+EVEIVGIR T KTTVTGVEMFRK L+G+RGN+G L+RG ++ VERG +LCK
 Sbjct: 233 IVKVGEEVEIVGIRPTS KTTVTGVEMFRKLLDQGQAGDNIGALVRGVTRDGVERGQILCK 292

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGS+ PKKFE E Y+L+KEEGGRHTPFFTNYRPQFY RTTDVTG ++LPEG EMVMPGD
 Sbjct: 293 PGSVKPHKKFMAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDVTGIVSLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNII 399
 NV + VEII P+A+E +FAIREGGRTVGAG+V++I+E
 Sbjct: 353 NVTVEVELIVPIAMEEKLRFAIREGGRTVGAGIVASIVE 391

Database: EXPASY/UniProtKB

Posted date: Jun 6, 2005 10:37 AM

Number of letters in database: 640,866,274

Number of sequences in database: 1,974,938

Lambda	K	H
0.315	0.135	0.383

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
length of query: 399
length of database: 640,866,274
effective HSP length: 128
effective length of query: 271
effective length of database: 388,074,210
effective search space: 105168110910
effective search space used: 105168110910
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (22.0 bits)
S2: 75 (33.5 bits)

Wallclock time: 18 seconds

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